



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 126127

TO: Dave Nguyen
Location: REM-2D31/2C18
Art Unit: 1632
Friday, July 02, 2004

Case Serial Number: 10/068160

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
Phone: 571-272-2518 *BOB*

barbara.obryen@uspto.gov

Search Notes

Ex. Nguyen,

Part 1 of your search could only be done in the Registry file. Results are expensive to display there, so I pulled out the GenBank hits & printed those records ~~def~~ directly from GenBank. The GenBank printouts are behind the STN printouts.

Please let me know if you have any questions.

Barb



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg.



GenCore version 5.1.6
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CM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:11:05 ; Search time 138.732 Seconds
(without alignments)
625.926 Million cell updates/sec

Title: US-10-068-160-20

Perfect score: 18

Sequence: 1 tgcgtcggtgcaggggg 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0

Maximum DB seq length: 2080000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/FCI_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	15	US-10-068-160-20
2	18	100.0	20	17	US-10-068-022-8
3	17	94.4	19	15	US-10-194-035-79
4	16.4	91.1	18	15	US-10-068-160-16
5	16.4	91.1	20	15	US-10-068-160-7
6	16.4	91.1	20	15	US-10-194-035-40
7	16.4	91.1	20	15	US-10-194-035-81
8	16.4	91.1	20	15	US-10-194-035-82
9	16.4	91.1	20	17	US-10-666-022-4
10	16.4	91.1	20	17	US-10-666-022-16
11	16	88.9	840	9	US-09-960-631A-1
12	16	88.9	1392	9	US-09-822-830A-199
13	16	88.9	2487	17	US-10-416-314-99
14	15.4	85.6	19	15	US-10-194-035-75

15	15.4	85.6	19	15	US-10-194-035-83	Sequence 83, Appl
16	15.4	85.6	303	13	US-10-424-599-125602	Sequence 125602, A
c 17	15.4	85.6	570	13	US-10-424-599-82230	Sequence 82230, A
18	15.4	85.6	765	9	US-09-974-300-7185	Sequence 7185, Ap
c 19	15.4	85.6	815	13	US-10-424-599-97884	Sequence 97884, A
c 20	15.4	85.6	1842	17	US-10-437-963-10345	Sequence 10345, A
c 21	15.4	85.6	2772	17	US-10-437-963-14876	Sequence 14876, A
22	15.4	85.6	2859	13	US-10-282-1228-27811	Sequence 27811, A
c 23	15.4	85.6	3162	13	US-10-027-632-114523	Sequence 114523, A
c 24	15.4	85.6	3162	16	US-10-027-632-114523	Sequence 114523, A
25	15	83.3	476	17	US-10-437-963-98704	Sequence 98704, A
26	15	83.3	1007	16	US-10-369-493-32802	Sequence 32802, A
27	15	83.3	1463	17	US-10-437-963-45745	Sequence 45745, A
c 28	15	83.3	1590	17	US-10-437-963-90205	Sequence 90205, A
c 29	15	83.3	1868	17	US-10-437-963-84855	Sequence 84855, A
c 30	15	83.3	1923	17	US-10-437-963-90203	Sequence 90203, A
31	15	83.3	2000	16	US-10-260-238-2666	Sequence 2666, Ap
32	15	83.3	2448	15	US-10-349-836-13	Sequence 13, Appl
33	15	83.3	2450	9	US-09-892-985-9	Sequence 9, Appl
34	15	83.3	18435	15	US-10-156-761-412	Sequence 412, App
35	15	83.3	100000	15	US-10-156-761-15103	Sequence 15103, A
c 36	15	83.3	9025608	15	US-10-156-761-1	Sequence 1, Appl
37	14.8	82.2	18	13	US-09-874-991C-503	Sequence 503, App
38	14.8	82.2	18	13	US-09-874-991C-513	Sequence 513, App
39	14.8	82.2	18	13	US-09-874-991C-551	Sequence 551, App
40	14.8	82.2	18	15	US-10-068-160-12	Sequence 12, Appl
41	14.8	82.2	18	15	US-10-068-160-13	Sequence 13, Appl
42	14.8	82.2	18	15	US-10-068-160-14	Sequence 14, Appl
43	14.8	82.2	18	15	US-10-068-160-17	Sequence 17, Appl
44	14.8	82.2	18	15	US-10-068-160-18	Sequence 18, Appl
45	14.8	82.2	20	13	US-09-874-991C-494	Sequence 494, App

ALIGNMENTS

RESULT 1
US-10-068-160-20
; Sequence 20, Application US/10068160
; Publication No. US2003006040A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: DANIELA
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068.160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-20

Query Match 100.0% Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No; 40;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCCTCGGTGCAGGGGG 18
| | | | | | | | | | | | | | | | | |
Db 1 TGCCTCGGTGCAGGGGG 18

RESULT 2
US-10-666-022-8

; Sequence 8, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Kliman, Dennis M.
; APPLICANT: Verthelyi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: misc feature
; LOCATION: (1)-(20)
; OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-8

Query Match 100.0%; Score 18; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGCTCGGTCAGGGGG 18
DB 3 TGGCTCGGTCAGGGGG 20

RESULT 3
US-10-194-035-79
; Sequence 79, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLIMAN, DENNIS
; APPLICANT: ISHII, KEN
; APPLICANT: VERHELVI, DANIELA
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-79

Query Match 94.4%; Score 17; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGCTCGGTCAGGGGG 17
DB 3 TGGCTCGGTCAGGGGG 19

RESULT 4
US-10-068-160-16
; Sequence 16, Application US/10068160
; Publication No. US2003006040A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLIMAN, DENNIS
; APPLICANT: ISHII, KEN
; APPLICANT: VERHELVI, DANIELA
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-16

Query Match 91.1%; Score 16.4; DB 15; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCTCGGTCAGGGGG 18
DB 1 TGGCTCGGTCAGGGGG 18

RESULT 5
US-10-068-160-7
; Sequence 7, Application US/10068160
; Publication No. US2003006040A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLIMAN, DENNIS
; APPLICANT: ISHII, KEN
; APPLICANT: VERHELVI, DANIELA
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-7

Query Match 91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCTCGGTCAGGGGG 18
DB 3 TGGCTCGGTCAGGGGG 20

RESULT 6
US-10-194-035-40


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; Sequence 40, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERHELHI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-40

Query Match          91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGCGTCGACGGGGG 18
   ||||| ||||| ||||| |||||
Db 3 TCGTCGATGCAGGGGGG 20

RESULT 7
US-10-194-035-81
; Sequence 81, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERHELHI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 81
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-81

Query Match          91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGCGTCGACGGGGG 18
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Db 3 TCGTCGATGCAGGGGGG 20

RESULT 8
US-10-194-035-81
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US-10-194-035-82
; Sequence 82, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERHELHI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-82

Query Match          91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGCGTCGACGGGGG 18
   ||||| ||||| ||||| |||||
Db 3 TCGTCGATGCAGGGGGG 20

RESULT 9
US-10-666-022-4
; Sequence 4, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, as represented by the
; SECRETARY of the Department of Health and Human Services
; APPLICANT: Kliman, Dennis M.
; APPLICANT: Verhelhi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISE;
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: misc feature
; LOCATION: (1)-(20)
; OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-4

Query Match          91.1%; Score 16.4; DB 17; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGCGTCGACGGGGG 18
   ||||| ||||| ||||| |||||
Db 3 TCGTCGATGCAGGGGGG 20
```

RESULT 10

US-10-666-022-16
; Sequence 16, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Kliman, Dennis M.
; APPLICANT: Verheij, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-666-022-16

Query Match 91.1%; Score 16.4; DB 17; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCTCGGTGCAGGGGG 18
| | | | | | | | | | | | | | | | | | | |
Db 3 TGGCTCGATGCAGGGGG 20

RESULT 11

US-09-960-631A-1
; Sequence 1, Application US/09960631A
; Patent No. US20020160495A1
; GENERAL INFORMATION:
; APPLICANT: MIROCHNITCHENKO, Oleg
; APPLICANT: Wei, Jiang
; TITLE OF INVENTION: SOLUBLE ISCHEMIA ACTIVATED PROTEIN
; FILE REFERENCE: 266/171
; CURRENT APPLICATION NUMBER: US/09/960,631A
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/233,819
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-960-631A-1

Query Match 88.9%; Score 16; DB 9; Length 840;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGGGG 17
| | | | | | | | | | | | | | | | | | | |
Db 12 GCGTCGGTGCAGGGGG 27

RESULT 12

US-09-822-830A-199/c
; Sequence 199, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:

; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalak
; APPLICANT: Graham, James R.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 1192
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-830A-199

Query Match 88.9%; Score 16; DB 9; Length 1192;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGGGG 17
| | | | | | | | | | | | | | | | | | | |
Db 376 GCGTCGGTGCAGGGGG 361

RESULT 13

US-10-416-314-99
; Sequence 99, Application US/10416314
; Publication No. US20040082508A1
; GENERAL INFORMATION:
; APPLICANT: YUE, Henry
; APPLICANT: YAO, Monique G.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: SWARNAKAR, Anita
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: SANJANWALA, Madhusudan M.
; APPLICANT: THORNTON, Michael B.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: LU, Yan
; APPLICANT: GIETZEN, Kimberly J.
; APPLICANT: BURFORD, Neil
; APPLICANT: DING, Li
; APPLICANT: TANG, Y. Tom
; APPLICANT: HAPALIA, April J.A.
; APPLICANT: BANDMAN, Olga
; APPLICANT: WARREN, Bridget A.
; APPLICANT: HONCHELL, Cynthia D.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: LEE, Sally
; APPLICANT: XU, Yuming
; APPLICANT: YANG, Junning
; APPLICANT: LAL, Preeti G.
; APPLICANT: TRAN, Bao
; APPLICANT: ISON, Craig H.
; APPLICANT: DUGGAN, Brendan M.
; APPLICANT: KAREHT, Stephanie K.
; TITLE OF INVENTION: SECRETED PROTEINS
; FILE REFERENCE: PI-0287 USN
; CURRENT APPLICATION NUMBER: US/10/416,314
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/247,505
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/249,642
; PRIOR FILING DATE: 2000-11-09

; PRIOR APPLICATION NUMBER: US 60/249,824
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/252,824
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 60/254,305
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/256,448
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PERL Program
; SEQ ID NO 99
; LENGTH: 2487
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 1545079CBI
US-10-416-314-99

Query Match 88.9%; Score 16; DB 17; Length 2487;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGTCGACGGGG 17
|||||
DB 675 GCGTCGTCGACGGGG 690

RESULT 14
US-10-194-035-75
; Sequence 75, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-75

Query Match 85.6%; Score 15.4; DB 15; Length 19;
Best Local Similarity 94.1%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGTCGACGGGG 17
|||||
DB 3 TCGTCGTCGACGGGG 19

RESULT 15
US-10-194-035-83
; Sequence 83, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis

; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-83

Query Match 85.6%; Score 15.4; DB 15; Length 19;
Best Local Similarity 94.1%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGTCGACGGGG 17
|||||
DB 3 TCGTCGTCGACGGGG 19

Search completed: July 2, 2004, 13:58:31
Job time : 143.732 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:38:45 ; Search time 1348.02 seconds

(without alignments)
398.746 Million cell updates/sec

Title: US-10-068-160-20

Perfect score: 18

Sequence: 1 tgcgtcggtgcaggggg 18

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 27513289 seqs, 1493109276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmi:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_nam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rtd:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	16.4	91.1	245	10 AW325275	AW325275 TENU4637
c 2	16.4	91.1	271	29 CE174729	CE174729 tigr-gss-
c 3	16.4	91.1	277	28 AQ444154	AQ444154 GSSTC0207
c 4	16.4	91.1	323	9 AL898002	AL898002 AL898002

5	16.4	91.1	400	12	BJ216073
6	16.4	91.1	421	9	AL897989
c 7	16.4	91.1	429	28	BH746584
c 8	16.4	91.1	1018	12	BG913279
c 9	16.4	91.1	1110	29	AG082246
10	16.4	91.1	1173	29	AG121475
11	16.4	91.1	1404	28	BZ554593
c 12	16	88.9	415	12	BM068740
c 13	16	88.9	453	12	BM055266
c 14	16	88.9	490	12	BM792946
c 15	16	88.9	519	12	BM820521
c 16	16	88.9	677	10	BF983122
c 17	16	88.9	697	12	BG493894
c 18	16	88.9	762	10	BE275117
c 19	16	88.9	787	14	CB990992
c 20	16	88.9	788	14	CB961467
c 21	16	88.9	791	29	CG343610
c 22	16	88.9	808	29	CG284584
c 23	16	88.9	809	14	CB988391
c 24	16	88.9	815	10	BE910177
c 25	16	88.9	826	29	CG316705
c 26	16	88.9	842	12	BG419606
c 27	16	88.9	853	14	CB997838
c 28	16	88.9	863	9	AL562129
c 29	16	88.9	867	14	CB988924
c 30	16	88.9	876	14	CD110248
c 31	16	88.9	880	13	BUI94354
c 32	16	88.9	923	29	CG284593
c 33	16	88.9	936	13	BX403217
c 34	16	88.9	945	29	CG316713
c 35	16	88.9	974	12	BG749183
c 36	16	88.9	996	13	BX339259
c 37	16	88.9	1005	13	BX384032
c 38	16	88.9	1026	13	BUI56800
c 39	16	88.9	1063	13	BQ921007
c 40	16	88.9	1085	14	CB992782
c 41	16	88.9	1088	14	CD107371
c 42	16	88.9	1098	13	BX377620
c 43	16	88.9	1099	13	BUI527443
c 44	16	88.9	1114	13	BQ439272
c 45	16	88.9	1132	12	BMS51929

ALIGNMENTS

RESULT 1
AW325275/c
LOCUS
DEFINITION
TENU4637 T.cruzi epimastigote normalized cDNA Library Trypanosoma
cruzi CDNA clone 25h9 5', mRNA sequence.
ACCESSION
AW325275
VERSION
AW325275.1 GI:6761196
KEYWORDS
EST.
SOURCE
Trypanosoma cruzi
ORGANISM
Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
REFERENCE
1 (bases 1 to 245)
AUTHORS
Porcel, B.M., Tran, A.-N., Tammi, M., Nyarady, Z., Rydaker, M.,
Umenyi, T.P., Rondinelli, E., Pettersson, U., Andersson, B. and
Aslund, L.
TITLE
Gene survey of the pathogenic protozoan Trypanosoma cruzi
JOURNAL
Genome Res. 10 (8), 1103-1107 (2000)
MEDLINE
20414748
PUBMED
10958628
COMMENT
Contact: Aslund L
Department of Medical Genetics
Uppsala University
Biomedical Center, Box 589, S-751 23 Uppsala, Sweden
Tel: 46 18 471 45 85
Fax: 46 18 52 68 49
Email: lena.aslund@medgen.uu.se

```

Seq primer: T7 primer
High quality sequence stop: 245.
Location/Qualifiers
1. .245
/organism="Trypanosoma cruzi"
/mol_type="mRNA"
/strain="Cl-Brenner"
/db_xref="taxon:5693"
/clone="25h9"
/cell_type="epimastigote"
/clone_lib="T. cruzi epimastigote normalized cDNA Library"
/notes="cDNA library constructed with oligo dt primed
epimastigote mRNA and cloned in pT7-318D phagemid with
modified polylinker (Pharmacia)"

ORIGIN
Query Match 91.1%; Score 16.4; DB 10; Length 245;
Best Local Similarity 94.4%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGTCGGTGCAGGGGG 18
Db 65 TGCATCGGTGCAGGGGG 48

RESULT 2
LOCUS CE174729
DEFINITION tigr-gss-dog-17000326716213 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE174729
VERSION CE174729.1 GI:35318341
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE 1 (bases 1 to 271)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
Kirness, E.F., Batina, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J. C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
22875432
14512627
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
FEATURES
source
Location/Qualifiers
1. .271
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 91.1%; Score 16.4; DB 29; Length 271;
Best Local Similarity 94.4%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGTCGGTGCAGGGGG 18
Db 217 TGGTCGGTGCAGGGGG 234

RESULT 3
LOCUS AQ444154/c
DEFINITION AQ444154 Trypanosoma cruzi random genomic library Trypanosoma
cruzi genomic clone G10L7, genomic survey sequence.
ACCESSION AQ444154
VERSION AQ444154.3 GI:10130745
KEYWORDS GSS.
SOURCE Trypanosoma cruzi
ORGANISM Trypanosoma cruzi
REFERENCE 1 (bases 1 to 277)
AUTHORS Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
Agüero, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.
A random sequencing approach for the analysis of the trypanosoma
cruzi genome: General structure, large gene and repetitive DNA
families, and gene discovery
Genome Res. 10 (12), 1996-2005 (2000)
20568489
11116094
On Sep 14, 2000 this sequence version replaced gi:9372108.
Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnológicas (Univ. Nac. de Gral
San Martín)
Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martín, Buenos
Aires, Argentina
Tel: (54-11) 4580/7255/7
Fax: (54-11) 4752-9639
Email: dsanchez@lib.unsam.edu.ar
Sequences were basecalled with phred and vector was masked with
crossmatch (see http://genome.washington.edu). Sequences were then
trimmed from both ends to remove low quality bases and masked
vector.
Seq primer: T7
Class: shotgun.
FEATURES
source
Location/Qualifiers
1. .277
/organism="Trypanosoma cruzi"
/mol_type="genomic DNA"
/strain="Cl-Brenner"
/db_xref="taxon:5693"
/clone="G10L7"
/cell_type="epimastigote"
/clone_lib="Trypanosoma cruzi random genomic library"
/notes="Vector: pBS(-) (Stratagene); T. cruzi DNA was
randomly sheared using a nebulizer and the 1 to 2 Kb range
was gel purified and cloned into the dephosphoryated
KincII site of the vector"

ORIGIN
Query Match 91.1%; Score 16.4; DB 28; Length 277;
Best Local Similarity 94.4%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGTCGGTGCAGGGGG 18
Db 238 TGCATCGGTGCAGGGGG 221

RESULT 4
LOCUS AL898002
DEFINITION AL898002 XGC-egg Silurana tropicalis cDNA clone TEGg043g16 5', mRNA
sequence.
ACCESSION AL898002
VERSION AL898002.2 GI:38697559
KEYWORDS EST.
SOURCE Silurana tropicalis (western clawed frog)
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Silurana.
REFERENCE 1 (bases 1 to 323)

```

AUTHORS Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
 TITLE Sanger Xenopus tropicalis EST project 2001 (11_2003)
 JOURNAL Unpublished (2003)
 COMMENT On Sep 16, 2002 this sequence version replaced gi:22950395.

Contact: Taylor R
 Sanger Institute
 Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: trop@sanger.ac.uk
 Sanger Xenopus tropicalis EST project 2001
 TROPICALIS_SEQUENCE_ID: TEGG043916.plkSP6
 Sequencing primer: SP6
 This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn.
 cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
 EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
 5' end and NotI at the 3' end.
 Vector: pCS107; Site 1: EcoRI; Site 2: NotI
 Host: Escherichia coli XL1-blue.
 Location/Qualifiers

FEATURES

source
 1..323
 /organism="Silurana tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="TEGG043916"
 /dev_stage="egg"
 /lab_host="Escherichia coli XL1-blue"
 /clone_lib="XGC-egg"
 /note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
 was oligo dT primed from 5ug of poly A+ RNA from egg.
 EcoRI-NotI cut cDNA was then ligated into pCS107 with
 EcoRI at the 5' end and NotI at the 3' end"

ORIGIN

Query Match 91.1%; Score 16.4; DB 9; Length 323;
 Best Local Similarity 94.4%; Pred. No. 1.5e+04;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCCTCGGTGCAGGGGGG 18
 |||||
 DB 79 TGCCTCGGTGCAGGGGGG 96

RESULT 5
 BJ216073
 LOCUS BJ216073 Y. Ogihara unpublished cDNA library, Wh Triticum aestivum
 DEFINITION BJ216073 400 bp mRNA linear EST 17-SEP-2002
 cDNA clone wh9n06 3', mRNA sequence.
 ACCESSION BJ216073
 VERSION BJ216073.1 GI:23071352
 KEYWORDS EST
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 400)
 Ogihara, Y. and Murai, K.
 Expressed Genes in Triticum aestivum
 Unpublished (2002)
 Contact: Tadao Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tsun@genes.nig.ac.jp.
 Location/Qualifiers

FEATURES

source
 1..400
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultiVar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="wh9n06"

ORIGIN
 /tissue_type="spike at meiosis"
 /dev_stage="feekes", scale 9"
 /clone_lib="Y. Ogihara unpublished cDNA library, Wh"

Query Match 91.1%; Score 16.4; DB 12; Length 400;
 Best Local Similarity 94.4%; Pred. No. 1.5e+04;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCCTCGGTGCAGGGGGG 18
 |||||
 DB 372 TGCCTCGGTGCAGGGGGG 389

RESULT 6

AL897989
 LOCUS AL897989 XGC-egg Silurana tropicalis cDNA clone TEGG043e14 5', mRNA
 DEFINITION AL897989 sequence.

ACCESSION AL897989
 VERSION AL897989.2 GI:38697548
 KEYWORDS EST.
 SOURCE Silurana tropicalis (western clawed frog)
 ORGANISM Silurana tropicalis
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 Xenopodinae; Silurana.

REFERENCE 1 (bases 1 to 421)
 Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
 Sanger Xenopus tropicalis EST project 2001 (11_2003)
 TITLE Sanger Xenopus tropicalis EST project 2001 (11_2003)
 JOURNAL Unpublished (2003)
 COMMENT On Sep 16, 2002 this sequence version replaced gi:22950382.
 Contact: Taylor R
 Sanger Institute
 Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: trop@sanger.ac.uk
 Sanger Xenopus tropicalis EST project 2001
 TROPICALIS_SEQUENCE_ID: TEGG043e14.plkSP6
 Sequencing primer: SP6
 This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn.
 cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
 EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
 5' end and NotI at the 3' end.
 Vector: pCS107; Site 1: EcoRI; Site 2: NotI
 Host: Escherichia coli XL1-blue.
 Location/Qualifiers

FEATURES

source
 1..421
 /organism="Silurana tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="TEGG043e14"
 /dev_stage="egg"
 /lab_host="Escherichia coli XL1-blue"
 /clone_lib="XGC-egg"
 /note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
 was oligo dT primed from 5ug of poly A+ RNA from egg.
 EcoRI-NotI cut cDNA was then ligated into pCS107 with
 EcoRI at the 5' end and NotI at the 3' end"

ORIGIN

Query Match 91.1%; Score 16.4; DB 9; Length 421;
 Best Local Similarity 94.4%; Pred. No. 1.5e+04;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCCTCGGTGCAGGGGGG 18
 |||||
 DB 79 TGCCTCGGTGCAGGGGGG 96

RESULT 7

BH746584/c
 LOCUS BH746584 429 bp DNA linear GSS 27-FEB-2002

```

DEFINITION SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.
ACCESSION BH746584
VERSION BH746584.1 GI:18959699
SOURCE GSS.
ORGANISM Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 429)
AUTHORS Alonzo, J.M., Leisse, T.J., Barajas, F., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karne, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J., and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At1g42480.
Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source           1..429
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_044872.30.00.x"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains one or more TDNA insertion
                     elements. The resultant fragment for each line was
                     directly sequenced to determine the genomic sequence at
                     the site of insertion. Details of the protocols used can
                     be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match          91.1%; Score 16.4; DB 28; Length 429;
Best Local Similarity 94.4%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCTCGTGCAGGGGGG 18
||||| |||||||
Db 414 TGCCTCGTGCAGGGGGG 397

RESULT 8
BG913279/c
LOCUS BG913279 1018 bp mRNA linear EST 05-JUN-2001
DEFINITION 602811967F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4943992
5', mRNA sequence.
ACCESSION BG913279
VERSION BG913279.1 GI:14293755
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1018)
AUTHORS NIH-WGC http://ngc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.

```

```

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10888 row: e column: 17
High quality sequence stop: 472.
FEATURES             Location/Qualifiers
     source           1..1018
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4943992"
                     /tissue_type="anaplastic oligodendroglioma with ip/19q
                     loss"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI CGAP Brn67"
                     /note="Organ: brain; Vector: PCMV-SPORT6; Site: 1; NotI;
                     Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 2.3 kb. Constructed by Life
                     Technologies. Note: this is a NCI CGAP Library."

ORIGIN
Query Match          91.1%; Score 16.4; DB 12; Length 1018;
Best Local Similarity 94.4%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCTCGTGCAGGGGGG 18
||||| |||||||
Db 751 TCGCTCGTGCAGGGGGG 734

RESULT 9
AG082246/c
LOCUS AG082246 1110 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-079807.R, genomic survey sequence.
ACCESSION AG082246
VERSION AG082246.1 GI:16634048
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1110)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpansegsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
FEATURES             Location/Qualifiers
     source           1..1110
                     /organism="pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="PTB-079807.R"
                     /sex="male"

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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match          91.1%; Score 16.4; DB 29; Length 1110;
Best Local Similarity 94.4%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCTCGGTGCAGGGGG 18
||||| ||||| ||||| |||||
Db 611 TGGCTGCTGCAGGGGG 594

RESULT 10
AG121475
LOCUS Pan troglodytes DNA, clone: PTB-130114.F, genomic survey sequence.
DEFINITION AG121475
ACCESSION AG121475.1 GI:16650640
VERSION
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
AUTHORS Totoki, Y., Watanabe, H., and Sakaki, Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1173)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
{E-mail: chimpanzee@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170}
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI
FEATURES
Location/Qualifiers
1..1173
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-130114.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match          91.1%; Score 16.4; DB 29; Length 1173;
Best Local Similarity 94.4%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCTCGGTGCAGGGGG 18
||||| ||||| ||||| |||||
Db 910 TGGCTGCTGCAGGGGG 927

RESULT 11
BZ554593
LOCUS Pseudomonas aeruginosa
DEFINITION pacsl-60 Pseudomonas aeruginosa genomic clone
pacsl-60 4763, genomic survey sequence.
ACCESSION BZ554593

/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match          91.1%; Score 16.4; DB 29; Length 1110;
Best Local Similarity 94.4%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCTCGGTGCAGGGGG 18
||||| ||||| ||||| |||||
Db 611 TGGCTGCTGCAGGGGG 594

RESULT 10
AG121475
LOCUS Pan troglodytes DNA, clone: PTB-130114.F, genomic survey sequence.
DEFINITION AG121475
ACCESSION AG121475.1 GI:16650640
VERSION
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
AUTHORS Totoki, Y., Watanabe, H., and Sakaki, Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1173)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
{E-mail: chimpanzee@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170}
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI
FEATURES
Location/Qualifiers
1..1173
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-130114.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match          91.1%; Score 16.4; DB 29; Length 1173;
Best Local Similarity 94.4%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCTCGGTGCAGGGGG 18
||||| ||||| ||||| |||||
Db 910 TGGCTGCTGCAGGGGG 927

RESULT 11
BZ554593
LOCUS Pseudomonas aeruginosa
DEFINITION pacsl-60 Pseudomonas aeruginosa genomic clone
pacsl-60 4763, genomic survey sequence.
ACCESSION BZ554593

/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match          91.1%; Score 16.4; DB 28; Length 1404;
Best Local Similarity 94.4%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCTCGGTGCAGGGGG 18
||||| ||||| ||||| |||||
Db 760 TCGCTCGGTGCAGGGGG 777

RESULT 12
BM068740
LOCUS ie84c05.y1 Melton Normalized Human Islet 4 M4-HIS 1 Homo sapiens
CDNA clone IMAGE:5673585 5', mRNA sequence.
ACCESSION BM068740
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kastner, K.,
AUTHORS Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blisstein, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Teagareishvili, R.,
Williams, T., Jackson, Y., and Bowers, Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: ie84c05.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohpc.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on

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BZ554593.1 GI:27162271
GSS.
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1404)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
Location/Qualifiers
1..1404
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="1-60"
/db_xref="taxon:287"
/clone="pacsl-60 4763"
/clone_lib="pacsl-60"
/note="clinical isolate 1-60 Whole genomic shotgun
library."

ORIGIN
Query Match          91.1%; Score 16.4; DB 28; Length 1404;
Best Local Similarity 94.4%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCTCGGTGCAGGGGG 18
||||| ||||| ||||| |||||
Db 760 TCGCTCGGTGCAGGGGG 777

RESULT 12
BM068740
LOCUS ie84c05.y1 Melton Normalized Human Islet 4 M4-HIS 1 Homo sapiens
CDNA clone IMAGE:5673585 5', mRNA sequence.
ACCESSION BM068740
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
AUTHORS Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blisstein, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Teagareishvili, R.,
Williams, T., Jackson, Y., and Bowers, Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: ie84c05.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohpc.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on

```


obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
High quality sequence stop: 413.

FEATURES

Location/Qualifiers
1..415
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5673585"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/note="Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1;
Site 2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

ORIGIN

Query Match 88.9%; Score 16; DB 12; Length 415;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGTCGACGGGG 17
|||||
DB 101 GCGTCGTCGACGGGG 86

RESULT 13

BM055266/c
LOCUS BM055266 453 bp mRNA linear EST 12-MAR-2002
DEFINITION t92f10.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:5674507 5', mRNA sequence.

ACCESSION BM055266
VERSION BM055266.1 GI:16913022
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 453)

REFERENCE
AUTHORS

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Renko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R.,
Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)

TITLE
JOURNAL

COMMENT
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557

Email: dmelton@biohpc.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE

consortium, for clone orders contact: info@image.llnl.gov
High quality sequence stop: 429.

FEATURES

Location/Qualifiers
1..453
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5674507"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/note="Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1;
Site 2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

ORIGIN

Query Match 88.9%; Score 16; DB 12; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGTCGACGGGG 17
|||||
DB 325 GCGTCGTCGACGGGG 310

RESULT 14

BM792946/c
LOCUS BM792946 490 bp mRNA linear EST 05-MAR-2002
DEFINITION K-EST0073583 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-4-D03
5', mRNA sequence.

ACCESSION BM792946
VERSION BM792946.1 GI:19141178
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 490)

REFERENCE
AUTHORS

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)

TITLE
JOURNAL

COMMENT
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 row: D column: 03

High quality sequence stop: 490.

Location/Qualifiers
1..490

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S22SNU16n1-4-D03"
/sex="F"
/tissue_type="Ascites"

/cell_type="Lymphoblast-like"
 /cell_line="SNU-16"
 /lab_host="DH10B"
 /clone_lib="S22SNU16n1"
 /notes="Organ: Stomach; Vector: pT7T3-Pac; Site 1: ECORI;
 Site 2: NotI; The S22SNU16 library was contributed by the
 Soares laboratory and it was constructed as described by
 Bonaldi, M.F., Lennon, G. and Soares, M.B. (1996), genome
 Research 6(9): 791-806. RNA was prepared from harvested
 cells of SNU-16 culture. SNU-16 cell was obtained from
 Korean Cell Line Bank (KCLB). SNU-16 was established from
 ascitic fluids of Korean patients by Park J.G. et al.
 (1990), Cancer Res 50: 2773-2780."

ORIGIN

Query Match 88.9%; Score 16; DB 12; Length 490;
 Best Local Similarity 100.0%; Pred. No. 2.2e+04;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGGG 17
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 DB 41 GCGTCGGTGCAGGGG 26

RESULT 15

BM820521/c
 LOCUS K-EST0089071 S20T655307 Homo sapiens cDNA clone S20T655307-7-H11
 DEFINITION 519 bp mRNA linear EST 06-MAR-2002

ACCESSION BM820521

VERSION BM820521.1 GI:19176934

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 519)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 7 row: H column: 11

High quality sequence stop: 519.

Location/Qualifiers

1..519

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S20T655307-7-H11"

/sex="M"

/lab_host="Top10F"

/clone_lib="S20T655307"

/notes="Organ: Stomach; Vector: pcNS; Site 1: ECORI;

Site 2: NotI; The poly (A)+ RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then decapped

with tobacco acid pyrophosphatase (TAP). The decapped

intact mRNA was ligated with DNA-RNA linker including EcoR

I site by treatment of T4 RNA ligase and the first strand

cDNA was synthesized from oligo dt-selected mRNA by

priming with dt-tailed vector. The dt-tailed vector was

adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transformation of

competent cells E. coli Top10F' by electroporation method.

The cDNA libraries constructed by this method are

full-length enriched cDNA library."

Query Match 88.9%; Score 16; DB 12; Length 519;

Best Local Similarity 100.0%; Pred. No. 2.2e+04;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGGG 17

|||||

DB 414 GCGTCGGTGCAGGGG 399

Search completed: July 2, 2004, 13:33:13
 Job time : 1350.14 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:09:30 ; Search time 28.2073 Seconds
(without alignments)
354.132 Million cell updates/sec

Title: US-10-068-160-20

Perfect score: 18
Sequence: 1 tgcgtcggtgcaggggg 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	15.4	85.6	885	4	US-09-252-991A-7532
C 2	15.4	85.6	912	4	US-09-252-991A-7811
C 3	15.4	85.6	1242	4	US-09-252-991A-7949
C 4	15.4	85.6	1392	4	US-09-489-039A-4664
C 5	15.4	85.6	1794	4	US-09-252-991A-7681
C 6	15	83.3	1521	1	US-08-486-855A-3
C 7	15	83.3	1521	2	US-07-938-154-9
C 8	15	83.3	1521	5	PCT-US91-02311-9
C 9	15	83.3	2448	4	US-08-487-596-13
C 10	15	83.3	2448	4	US-08-660-451A-13
C 11	15	83.3	2450	2	US-08-466-589-9
C 12	15	83.3	2450	2	US-08-700-636-9
C 13	15	83.3	2450	3	US-08-467-574-9
C 14	15	83.3	2450	4	US-09-217-345-9
C 15	15	83.3	2450	4	US-09-892-985-9
C 16	14.8	82.2	1814	4	US-09-702-705-319
C 17	14.8	82.2	1814	4	US-09-736-457-319
C 18	14.8	82.2	1814	4	US-09-614-124B-319
C 19	14.8	82.2	1814	4	US-09-671-325-319
C 20	14.8	82.2	1814	4	US-09-589-184-319
C 21	14.4	80.0	1584	4	US-09-489-039A-2524
C 22	14.4	80.0	43360	4	US-09-453-702B-206
C 23	14.4	80.0	45325	4	US-09-453-702B-261
C 24	14	77.8	227	1	US-08-337-268A-40
C 25	14	77.8	227	1	US-08-484-570A-40
C 26	14	77.8	876	4	US-09-252-991A-12753
C 27	14	77.8	36800	4	US-08-311-731A-139

C 28	13.8	76.7	402	4	US-09-252-991A-1377	Sequence 1877, Ap
C 29	13.8	76.7	423	4	US-09-252-991A-13029	Sequence 13029, A
C 30	13.8	76.7	552	4	US-09-252-991A-6091	Sequence 6091, Ap
C 31	13.8	76.7	609	4	US-09-252-991A-6173	Sequence 6173, Ap
C 32	13.8	76.7	633	4	US-09-489-039A-2752	Sequence 2752, Ap
C 33	13.8	76.7	642	4	US-09-252-991A-6014	Sequence 6014, Ap
C 34	13.8	76.7	822	4	US-09-252-991A-6377	Sequence 6377, Ap
C 35	13.8	76.7	861	4	US-09-252-991A-1836	Sequence 1836, Ap
C 36	13.8	76.7	883	3	US-08-943-731-171	Sequence 171, Ap
C 37	13.8	76.7	903	3	US-08-829-525-37	Sequence 37, Appl
C 38	13.8	76.7	903	3	US-08-609-583A-37	Sequence 37, Appl
C 39	13.8	76.7	903	3	US-08-937-399-37	Sequence 37, Appl
C 40	13.8	76.7	903	4	US-09-310-367-37	Sequence 37, Appl
C 41	13.8	76.7	903	4	US-09-032-337-37	Sequence 37, Appl
C 42	13.8	76.7	903	4	US-09-252-991A-8502	Sequence 8502, Ap
C 43	13.8	76.7	903	4	US-09-464-231-37	Sequence 37, Appl
C 44	13.8	76.7	1086	4	US-09-252-991A-8434	Sequence 8434, Ap
C 45	13.8	76.7	1110	4	US-09-252-991A-8962	Sequence 8962, Ap

ALIGNMENTS

RESULT 1
US-09-252-991A-7532/c
; Sequence 7532, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7532
; LENGTH: 885
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7532

Query Match 85.6%; Score 15.4; DB 4; Length 885;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGTCGTCACGGGGG 18
DB 642 GCGCGTCACGGGGG 626

RESULT 2
US-09-252-991A-7811
; Sequence 7811, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7811
; LENGTH: 912
; TYPE: DNA

ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7811

Query Match 85.6%; Score 15.4; DB 4; Length 912;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGGGG 18
||| ||||| ||||| |||||
DB 277 GCGGCGGTGCAGGGGG 293

RESULT 3

US-09-252-991A-7949
; Sequence 7949, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7949
; LENGTH: 1242
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7949

Query Match 85.6%; Score 15.4; DB 4; Length 1242;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGGGG 18
||| ||||| ||||| |||||
DB 509 GCGGCGGTGCAGGGGG 525

RESULT 4

US-09-489-039A-4664
; Sequence 4664, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489.039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 4664
; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (876)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-489-039A-4664

Query Match 85.6%; Score 15.4; DB 4; Length 1392;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGGGG 18
||| ||||| ||||| |||||

DB 335 GCTTCGGTGCAGGGGG 351

RESULT 5

US-09-252-991A-7681/c
; Sequence 7681, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7681
; LENGTH: 1794
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7681

Query Match 85.6%; Score 15.4; DB 4; Length 1794;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGGGG 18
||| ||||| ||||| |||||
DB 259 GCGGCGGTGCAGGGGG 243

RESULT 6

US-08-496-855A-3
; Sequence 3, Application US/08496855A
; Patent No. 5801232
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,855A
; FILING DATE: 20-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9369B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1521
OTHER INFORMATION: /note= "Human neuronal NACHR beta-2
OTHER INFORMATION: cDNA shown as top nucleotide sequence in
Figure..."
US-08-496-855A-3

Query Match 83.3%; Score 15; DB 1; Length 1521;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGG 16
|||||
DB 1192 GCGTCGGTGCAGGG 1206

RESULT 7

US-07-938-154-9
Sequence 9, Application US/07938154
Patent No. 5981193
GENERAL INFORMATION:
APPLICANT: Harpold, Michael M.
APPLICANT: Ellis, Stephen B.
APPLICANT: Brust, Paul
APPLICANT: Akong, Michael
APPLICANT: Velicelebi, Gonul
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty Schroeder Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/938,154
FILING DATE: 30-NOV-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US91/02311
FILING DATE: 03-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9380
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1521
OTHER INFORMATION: /note= "Human neuronal NACHR beta-2
OTHER INFORMATION: cDNA shown as top sequence in Fig 9."
US-07-938-154-9

Query Match 83.3%; Score 15; DB 2; Length 1521;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGG 16
|||||
DB 1192 GCGTCGGTGCAGGG 1206

RESULT 8

PCT-US91-02311-9
Sequence 9, Application PC/TUS9102311
GENERAL INFORMATION:
APPLICANT: Harpold, Michael M.
APPLICANT: Ellis, Stephen B.
APPLICANT: Brust, Paul
APPLICANT: Akong, Michael
APPLICANT: Velicelebi, Gonul
TITLE OF INVENTION: Human Neuronal Nicotinic Acetylcholine
Receptor Compositions and Methods Employing Same
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pich, Even, Tabin & Flannery
STREET: 135 S. LaSalle St.
CITY: Chicago
STATE: Ill.
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02311
FILING DATE: 19910403
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B.
REFERENCE/DOCKET NUMBER: 51247/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
PCT-US91-02311-9
Query Match 83.3%; Score 15; DB 5; Length 1521;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGG 16
|||||
DB 1192 GCGTCGGTGCAGGG 1206

RESULT 9

US-08-487-596-13
Sequence 13, Application US/08487596
Patent No. 6440681
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.

APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: METHODS FOR IDENTIFYING ACONISTS AND
TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/487,596
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US94/02447
FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,503
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9951
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2448 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 265..1773
OTHER INFORMATION: /product= "BETA-2 SUBUNIT"
US-08-487-596-13
Query Match 83.3%; Score 15; DB 4; Length 2448;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCCTCGGTGCAGGGG 16
DB 1444 GCCTCGGTGCAGGGG 1458
RESULT 10
US-08-660-451A-13
Sequence 13, Application US/08660451A
Patent No. 6524789
GENERAL INFORMATION:
APPLICANT: Elliott, Kathryn J.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,451A
FILING DATE: June 7, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,722
FILING DATE: 06/07/95
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2448 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 265..1773
OTHER INFORMATION: beta2 human neuronal nicotinic
acetylcholine receptor
NAME/KEY: 5'UTR
LOCATION: 1..264
OTHER INFORMATION:
NAME/KEY: 3'UTR
LOCATION: 1774..2448
OTHER INFORMATION:
US-08-660-451A-13
Query Match 83.3%; Score 15; DB 4; Length 2448;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCCTCGGTGCAGGGG 16
DB 1444 GCCTCGGTGCAGGGG 1458
RESULT 11
US-08-466-589-9
Sequence 9, Application US/08466589
Patent No. 5837489
GENERAL INFORMATION:
APPLICANT: Elliott, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

```
;
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,589
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9950
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2450 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 267..1775
; US-08-466-589-9

Query Match 83.3%; Score 15; DB 2; Length 2450;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCGTCGGTGCAGGGG 16
Db 1446 GCGTCGGTGCAGGGG 1460

RESULT 12
US-08-700-636-9
; Sequence 9, Application US/08700636
; Patent No. 5910582
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/700,636
; FILING DATE: 16-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2450 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 267..1775
; US-08-700-636-9

Query Match 83.3%; Score 15; DB 2; Length 2450;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCGTCGGTGCAGGGG 16
Db 1446 GCGTCGGTGCAGGGG 1460

RESULT 13
US-08-467-574-9
; Sequence 9, Application US/08467574
; Patent No. 6022704
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,574
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9949
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 2450 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 267..1775
US-08-467-574-9

Query Match      83.3%; Score 15; DB 3; Length 2450;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCGTCGGTGCAGGGG 16
Db      1446 GCGTCGGTGCAGGGG 1460

RESULT 14
US-09-217-345-9
; Sequence 9, Application US/09217345
; Patent No. 6303753
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2450 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 267..1775
US-08-467-574-9

Query Match      83.3%; Score 15; DB 3; Length 2450;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCGTCGGTGCAGGGG 16
Db      1446 GCGTCGGTGCAGGGG 1460

RESULT 14
US-09-217-345-9
; Sequence 9, Application US/09217345
; Patent No. 6303753
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
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; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
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; CORRESPONDENCE ADDRESS:
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; STREET: 4250 Executive Square, 7th Floor
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; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
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; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2450 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 267..1775
US-08-467-574-9

Query Match      83.3%; Score 15; DB 3; Length 2450;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCGTCGGTGCAGGGG 16
Db      1446 GCGTCGGTGCAGGGG 1460

RESULT 15
US-09-892-985-9
; Sequence 9, Application US/09892985
; Patent No. 6664375
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2450 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 267..1775
US-09-892-985-9

Query Match      83.3%; Score 15; DB 4; Length 2450;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCGTCGGTGCAGGGG 16
Db      1446 GCGTCGGTGCAGGGG 1460
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US-09-217-345-9

Query Match      83.3%; Score 15; DB 4; Length 2450;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCGTCGGTGCAGGGG 16
Db      1446 GCGTCGGTGCAGGGG 1460

RESULT 15
US-09-892-985-9
; Sequence 9, Application US/09892985
; Patent No. 6664375
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
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; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2450 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 267..1775
US-09-892-985-9

Query Match      83.3%; Score 15; DB 4; Length 2450;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCGTCGGTGCAGGGG 16
Db      1446 GCGTCGGTGCAGGGG 1460
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Db 1446 GCGTCGGTCACAGGG 1460

Search completed: July 2, 2004, 13:37:54
Job time : 29.2073 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 06:05:50 ; Search time 134.89 Seconds
(without alignments)
566.887 Million cell updates/sec

Title: US-10-068-160-20

Perfect score: 18

Sequence: 1 tgcgtcggtgcagg9999 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N.Geneseq_29Jan04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	18	100.0	20 7 ACC48318	Acc48318 CpG oligo
2	18	100.0	20 7 ACC48305	Acc48305 CpG oligo
3	18	100.0	20 8 ACC83123	Acc83123 D class C
4	17	94.4	13 4 AAC80659	Aac80659 Immunogen
5	17	94.4	19 4 AAS09629	Aas09629 Immunorea
6	17	94.4	19 6 ABK46507	Abk46507 Immunosti
7	16.4	91.1	20 4 AAC80662	Aac80662 Immunogen
8	16.4	91.1	20 4 AAC80661	Aac80661 Immunogen
9	16.4	91.1	20 4 AAC80620	Aac80620 Immunogen
10	16.4	91.1	20 4 AAS09631	Aas09631 Immunorea
11	16.4	91.1	20 4 AAS09590	Aas09590 Immunorea
12	16.4	91.1	20 4 AAS09632	Aas09632 Immunorea
13	16.4	91.1	20 6 ABK46510	Abk46510 Immunosti
14	16.4	91.1	20 6 ABK46468	Abk46468 Immunosti
15	16.4	91.1	20 6 ABK46509	Abk46509 Immunosti
16	16.4	91.1	20 7 ACC48298	Acc48298 CpG oligo
17	16.4	91.1	20 7 ACC48320	Acc48320 CpG oligo
18	16.4	91.1	20 7 ACC48312	Acc48312 CpG oligo
19	16.4	91.1	20 7 ACC48306	Acc48306 CpG oligo
20	16.4	91.1	20 7 ACC48319	Acc48319 CpG oligo
21	16.4	91.1	20 7 ACC48321	Acc48321 CpG oligo
22	16.4	91.1	20 8 ACC83125	Acc83125 D class C
23	16.4	91.1	20 8 ACC83117	Acc83117 D class C

24	16.4	91.1	20 8 ACC83124	Acc83124 D class C
25	16.4	91.1	20 8 ACC83126	Acc83126 D class C
26	16.4	91.1	20 9 ADD01050	Add01050 CpG D oli
27	16	88.9	840 7 ABX12764	Abx12764 DNA encod
28	16	88.9	1192 6 AAS62412	Aas62412 cDNA sequ
29	16	88.9	2487 6 AAL39655	Aal39655 Human sec
30	15.4	85.6	19 4 AAC80655	Aac80655 Immunogen
31	15.4	85.6	19 4 AAC80663	Aac80663 Immunogen
32	15.4	85.6	19 4 AAS09633	Aas09633 Immunorea
33	15.4	85.6	19 4 AAS09625	Aas09625 Immunorea
34	15.4	85.6	19 6 ABK46503	Abk46503 Immunosti
35	15.4	85.6	19 6 ABK46511	Abk46511 Immunosti
36	15.4	85.6	337 6 ABNL9459	Abnl9459 Human ORF
37	15.4	85.6	765 6 ABK79894	Abk79894 Bacillus
38	15.4	85.6	1510 9 ADC30295	Adc30295 Human nov
39	15.4	85.6	2118 5 AAS82471	Aas82471 DNA encod
40	15.4	85.6	2118 5 AAS93017	Aas93017 DNA encod
41	15.4	85.6	2859 7 ACA39941	Aca39941 Prokaryot
42	15.4	85.6	3290 7 ACF16998	Acf16998 Human NOV
43	15.4	85.6	12423 9 ADS54082	Ads54082 Pretreate
44	15	83.3	21 4 AAH62282	Aah62282 CHRN82 po
45	15	83.3	1023 9 ADB78681	Adb78681 Human nic

ALIGNMENTS

RESULT 1

ACC48318

ID ACC48318 standard; DNA; 20 BP.

XX AC ACC48318;

XX DT 11-AUG-2003 (first entry)

XX DB CpG oligodeoxynucleotide DV51.

XX KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;

XX KX cytotstatic; immunostimulant; gene therapy; ss.

XX OS Synthetic.

XX PN WO2003020884-A2.

XX PD 13-MAR-2003.

XX PF 13-AUG-2002; 2002WO-US025732.

XX PR 14-AUG-2001; 2001US-0312190P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX KI Kliman DM, Gursei M, Verthelyi D;

XX DR WPI; 2003-300874/29.

XX PT Generating mature dendritic cells for tumor immunotherapy or as vaccines for activating the immune system to treat diseases such as cancer, comprises contacting a dendritic cell precursor with a D type oligodeoxynucleotide.

XX PS Disclosure; Fig 8; 69pp; English.

XX CC The present sequence is that of CpG oligodeoxynucleotide DV51 of the invention. A claimed method for generating dendritic cells involves contacting a dendritic cell precursor, especially a monocyte, with a D type oligodeoxynucleotide (see ACC48294) containing a central unmethylated CpG motif. The method is useful for generating mature dendritic cells and enhancing T cell responses, thus enhancing antigen presentation. Mature dendritic cells are useful for tumour immunotherapy, for augmenting an immune response to an infectious agent or to a vaccine, and as vaccines to prevent future infection or to activate the immune system to treat diseases such as cancer. Mature dendritic cells may also

CC be used to produce activated T lymphocytes

XX Sequence 20 BP; 1 A; 3 C; 13 G; 3 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 18; DB 7; Length 20;

Best Local Similarity 100.0%; Pred. No. 68;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TGGGTGGGTGCAGGGGG 18

Db 3 TGGGTGGGTGCAGGGGG 20

RESULT 2

ACC48305

ID ACC48305 standard; DNA; 20 BP.

XX AC ACC48305;

XX DT 11-AUG-2003 (first entry)

XX DE CpG oligodeoxynucleotide used for dendritic cell maturation.

XX KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;

XX KW cytotatic; immunostimulant; gene therapy; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT misc_difference 1 /tag= a

FT /note= "N is any base (especially G) or no base"

FT misc_difference 2 /tag= b

FT /note= "N is any base (especially G) or no base"

XX WO2003020884-A2.

XX 13-MAR-2003.

XX 13-AUG-2002; 2002WO-US025732.

XX 14-AUG-2001; 2001US-0312190P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Klinman DM, Gursel M, Verthelyi D;

XX WPI; 2003-300874/29.

XX Generating mature dendritic cells for tumor immunotherapy or as vaccines

XX for activating the immune system to treat diseases such as cancer,

XX comprises contacting a dendritic cell precursor with a D type

XX oligodeoxynucleotide.

XX Disclosure; Page 26; 69pp; English.

XX The present sequence is that of a D type CpG oligodeoxynucleotide that is

XX an example of claimed D type oligodeoxynucleotides (see ACC48294) of the

XX invention. Mature dendritic cells are obtained by contacting a dendritic

XX cell precursor, such as a monocyte, with such an oligodeoxynucleotide.

XX The method is useful for generating mature dendritic cells and enhancing

XX T cell responses, thus enhancing antigen presentation. Mature dendritic

XX cells are useful for tumour immunotherapy, for augmenting an immune

XX response to an infectious agent or to a vaccine, and as vaccines to

XX prevent future infection or to activate the immune system to treat

XX diseases such as cancer. Mature dendritic cells may also be used to

XX produce activated T lymphocytes

XX SQ Sequence 20 BP; 1 A; 3 C; 11 G; 3 T; 0 U; 2 Other;

Query Match 100.0%; Score 18; DB 7; Length 20;

Best Local Similarity 100.0%; Pred. No. 68;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TGGGTGGGTGCAGGGGG 18

Db 3 TGGGTGGGTGCAGGGGG 20

RESULT 3

ACC83123

ID ACC83123 standard; DNA; 20 BP.

XX AC ACC83123;

XX DT 27-AUG-2003 (first entry)

XX DE D class CpG ODN sequence useful for encapsulating in SSCL, DV51.

XX KW Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;

XX KW tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;

XX KW thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;

XX KW schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;

XX KW asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;

XX KW CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;

XX KW multiple sclerosis; infection; tumour; ss.

XX OS Unidentified.

XX WO2003040308-A2.

XX 15-MAY-2003.

XX 29-JUL-2002; 2002WO-US024235.

XX 27-JUL-2001; 2001US-0308283P.

XX 25-JUL-2002; 2002US-00206407.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Klinman DM, Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK;

XX WPI; 2003-482260/45.

XX Cationic liposome composition for delivering oligodeoxynucleotides

XX including a CpG motif in clinical applications, comprises a cationic

XX lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.

XX Disclosure; Fig 10C; 110pp; English.

XX The invention relates to sterically stabilised cationic liposomes (SSCL)

XX which comprises a cationic lipid, a co-lipid, stabilising agent and

XX encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.

XX The invention is useful in pharmaceutical composition for impairing

XX growth of a solid tumour cell (e.g. human tumour cell) bearing an

XX interleukin-13 receptor in a subject; for stimulating an immune response,

XX which is expression of a cytokine (e.g. interferon gamma), particularly

XX immunotherapeutic response against tumours or stimulating an in vivo or

XX an in vitro immune cell, and for inducing an immune response against an

XX infectious agent e.g. virus, bacteria and fungus. It is also useful for

XX delivering oligodeoxynucleotides including a CpG motif in clinical

XX applications; for treating infectious diseases (e.g. tularemia, malaria,

XX francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer

XX (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer

XX etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,

XX bronchial or allergic asthma, urticaria, food allergies), autoimmune

XX diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and

XX multiple sclerosis) and psoriasis. The present sequence is a D class CpG

XX ODN potentially useful for encapsulating in SSCL

XX SQ Sequence 20 BP; 1 A; 3 C; 13 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 8; Length 20;

Best Local Similarity 100.0%; Pred. No. 68;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCGTGGTGCAGGGGG 18
 DB 3 TCGGTCGGTGCAGGGGG 20

RESULT 4
 ID AAC80659 standard; DNA; 19 BP.
 XX AAC80659;
 DT 14-FEB-2001 (first entry)
 DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:79.

KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
 KW immunogenic; cytokine release; natural killer cell; NK cell activation;
 KW cell-mediated immune response; T-cell response; humoral response;
 KW B-cell response; antibody production; immune response induction; vaccine;
 KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
 KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
 KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
 KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
 KW antimicrobial; anti-allergic; protozoicide; tuberculostatic;
 KW antiasthmatic; dermatological; phosphorothioate; ss.

OS Synthetic.
 XX WO200061151-A2.
 PN 19-OCT-2000.
 PD 12-APR-2000; 2000WO-US009839.
 PF 12-APR-1999; 99US-0128898P.
 PR (KLIN/) KLINMAN D.
 PA (ISHI/) ISHII K.
 PA (VERT/) VERTHELYI D.
 XX Klinman D, Ishii K, Verthelyi D;
 XX WPI; 2001-006880/01.
 DR Novel oligonucleotides useful for the prevention and treatment of
 PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
 PT resulting from exposure to a bio-warfare agent.
 XX Claim 4; Page 36; 46pp; English.

CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
 CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
 CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
 CC optionally have phosphorothioate linkages which make them more resistant
 CC to degradation. The invention also relates to an oligonucleotide delivery
 CC complex comprising an oligonucleotide of the invention and a targeting
 CC agent, and a pharmaceutical composition comprising the oligonucleotide
 CC delivery complex. The oligonucleotides are able to induce either a cell-
 CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
 CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g., macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergenic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic

CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antineoplastic therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention

XX
 SQ Sequence 19 BP; 1 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 94.4%; Score 17; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCGTGGTGCAGGGGG 17
 DB 3 TCGGTCGGTGCAGGGGG 19

RESULT 5
 AAS09629
 ID AAS09629 standard; DNA; 19 BP.
 XX AAS09629;
 AC AAS09629;
 DT 26-SEP-2001 (first entry)
 DE Immunoreactive CpG sequence-containing oligonucleotide #79.

KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergic; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antineoplastic therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW leishmania; Ebola; Anthrax; Listeria; ss.

OS Synthetic.
 XX WO200151500-A1.
 PN 19-JUL-2001.
 PD 12-JAN-2001; 2001WO-US001122.
 XX 14-JAN-2000; 2000US-0176115P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Klinman D, Ishii K, Verthelyi D;
 XX WPI; 2001-442129/47.

PT Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.
 XX Claim 5; Page 40; 48pp; English.
 XX AAS09551-AAS09562 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The

CC ODN are useful for inducing an immune response, preferably a cell-mediated immune response, involving non-B cell activation, interferon gamma (IFN-gamma) production or a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma, cancer, e.g. solid tumour cancer, a disease associated with the immune system e.g. autoimmune disorder or an immune system deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antineoplastic therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or colic, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines against hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, Anthrax and Listeria

XX Sequence 19 BP; 1 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 94.4%; Score 17; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGCGTCGACGGGG 17
| | | | | | | | | | | | | | | | | | |
Db 3 TCGTCGCGTCGACGGGG 19

RESULT 6

ID ABK46507
AC ABK46507; DNA; 19 BP.

XX

DT 05-JUN-2002 (first entry)

XX Immunostimulatory unmethylated CpG oligodeoxynucleotide #97.

XX unmethylated CpG; oligidideoxynucleotide; ODN; virucide; vaccine;

KW Paromyxoviridae; P protein; respiratory syncytial virus; RSV;

KW viral bronchiolitis; pneumonia; infectious pulmonary disease;

KW bronchopulmonary dysplasia; congenital heart condition; ss.

XX Synthetic.

OS WO200211761-A2.

PN 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US041633.

XX 10-AUG-2000; 2000US-0224011P.

XX 01-SEP-2000; 2000US-0229307P.

XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

XX Mond JU, Prince G, Klinman DM;

XX WPI; 2002-227118/28.

XX Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of Paromyxoviridae F protein, and cytosine followed by guanine linked by phosphate bond-oligodeoxynucleotides.

PS Claim 4; Page 9; 30pp; English.

XX The invention describes a vaccine comprising one or more epitopes of a Paromyxoviridae F protein, and one or more CpG (cytosine followed by guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The

CC vaccine is useful for vaccinating a patient especially against viruses of the Paromyxoviridae family e.g. respiratory syncytial virus (RSV), the primary cause of viral bronchiolitis and pneumonia in infants and children, and infectious pulmonary disease in infants. RSV has been particularly implicated in death of infants that are premature, have bronchopulmonary dysplasia, or congenital heart conditions. This sequence CC represents an oligodeoxynucleotide that can be used in the creation of the vaccine

XX Sequence 19 BP; 1 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 94.4%; Score 17; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGCGTCGACGGGG 17
| | | | | | | | | | | | | | | | | | |
Db 3 TCGTCGCGTCGACGGGG 19

RESULT 7

ID AAC80662
AC AAC80662; DNA; 20 BP.

XX

XX 14-FEB-2001 (first entry)

XX Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:82.

XX CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;

KW immunogenic; cytokine release; natural killer cell; NK cell activation;

KW cell-mediated immune response; T-cell response; humoral response;

KW B-cell response; antibody production; immune response induction; vaccine;

KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;

KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;

KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;

KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;

KW antimicrobial; antiallergic; protozoicide; tuberculostatic;

KW antiasthmatic; dermatological; phosphorothioate; ss.

XX Synthetic.

XX WO200061151-A2.

XX 19-OCT-2000.

XX 12-APR-2000; 2000WO-US009839.

XX 12-APR-1999; 99US-0128898P.

XX (KLIN/) KLINMAN D.

XX (ISHI/) ISHII K.

XX (VERT/) VERTHELYI D.

XX Klinman D, Ishii K, Verthelyi D;

XX WPI; 2001-006880/01.

XX Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent.

PS Claim 4; Page 36; 46pp; English.

XX The invention relates to novel immunogenic CpG oligodeoxynucleotides (AAC80581-C80723). The oligonucleotides are at least 10 bases long and comprise one of the generic sequences 5'-NNN-CpG-WNNN-3' or 5'-RY-CpG-RY-3'. The central CpG motif is unmethylated, and the oligonucleotides optionally have phosphorothioate linkages which make them more resistant to degradation. The invention also relates to an oligonucleotide delivery complex comprising an oligonucleotide of the invention and a targeting agent, and a pharmaceutical composition comprising the oligonucleotide

CC delivery complex. The oligonucleotides are able to induce either a cell-mediated (T-cell) response or a humoral (B-cell, antibody) response, with CC oligonucleotides of the sequence 5'-RV-CpG-RV-3', being able to induce a CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3' being able to induce a humoral response. It is thought that after CC administration, the oligonucleotide acts on antigen-presenting cells (e.g., macrophages and dendritic cells), which then release cytokines, CC leading to activation of natural killer (NK) cells. A cell-mediated or CC humoral response can then occur by activation of T- or B-cells. The CC induction of an immune response is useful for treating, preventing or CC ameliorating an allergic reaction (preferably asthma), or an infection, CC where an immunogenic CpG oligonucleotide is administered either alone or CC in combination with an anti-allergenic agent or anti-infectious agent. CC The allergic conditions which may be treated include eczema, allergic CC rhinitis, hayfever, urticaria, food allergies and other atopic CC conditions, and the infections which may be treated include viral, CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS, CC leishmania and schistosomiasis. Immune response induction may also be CC used in the treatment of an autoimmune disorder (e.g., lupus, CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease CC associated with immune system deficiency, and symptoms resulting from CC exposure to an agent of biological warfare. An immunogenic CpG CC oligonucleotide, either alone or in combination with an anti-cancer CC agent, is useful for treating solid tumour cancer. The induction of an CC immune response is used in antitense therapy and to improve the efficacy CC of a vaccine. The oligonucleotide is preferably administered to CC lymphocytes ex vivo, producing activated lymphocytes which are then CC administered to the host. The present sequence represents an immunogenic CC CpG oligodeoxynucleotide of the invention

XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 20;
Best Local Similarity 94.4%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGGTGGTGCAGGGGGG 18
|||||
Db 3 TGGGTGCATGCAGGGGG 20

RESULT 8

AAC80661

ID AAC80661 standard; DNA; 20 BP.

AC AAC80661;

DT 14-FEB-2001 (first entry)

DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:81.

XX CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
XX immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.

OS Synthetic.

XX WC2000061151-A2.

XX 19-OCT-2000.

XX 12-APR-2000; 2000WO-US0009839.

XX 12-APR-1999; 99US-0128988P.

XX (KLIN/) KLINMAN D.

PA (ISHI/) ISHII K.
XX (VERT/) VERTHELYI D.

PI Klinman D, Ishii K, Verthelyi D;

XX WPI; 2001-006880/01.

DR Novel oligonucleotides useful for the prevention and treatment of
XX allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.

XX Claim 4; Page 36; 46pp; English.

XX The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RV-CpG-RV-
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targeting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RV-CpG-RV-3', being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus, CC
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antitense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to CC
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention

XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 20;

Best Local Similarity 94.4%; Pred. No. 3.7e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGGTGGTGCAGGGGGG 18
|||||
Db 3 TGGGTGCATGCAGGGGG 20

RESULT 9

AAC80620

ID AAC80620 standard; DNA; 20 BP.

AC AAC80620;

DT 14-FEB-2001 (first entry)

DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:40.

XX CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;

XX immunogenic; cytokine release; natural killer cell; NK cell activation;
 XX cell-mediated immune response; T-cell response; humoral response;
 XX B-cell response; antibody production; immune response induction; vaccine;
 XX allergy; asthma; infection; bacterial; viral; fungal; protozoal;
 XX parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
 XX rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
 XX immune deficiency; biological warfare agent; cytostatic; antiarthritic;
 XX antimicrobial; antiallergic; protozoicide; tuberculostatic;
 XX antiasthmatic; dermatological; phosphorothioate; ss.

XX Synthetic.

XX WO200061151-A2.

XX 19-OCT-2000.

XX 12-APR-2000; 2000WO-US009839.

XX 12-APR-1999; 99US-0128898P.

XX (KLIN/) KLINMAN D.

XX (ISHI/) ISHII K.

XX (VERT/) VERTHELYI D.

XX Klinman D, Ishii K, Verthelyi D;

XX WPI; 2001-006880/01.

XX Novel oligonucleotides useful for the prevention and treatment of
 PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
 PT resulting from exposure to a bio-warfare agent.

XX Claim 4; Page 30; 46pp; English.

XX The invention relates to novel immunogenic CpG oligodeoxynucleotides
 CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
 CC comprise one of the generic sequences 5'-NNNT-CpG-WNN-3' or 5'-RY-CpG-RY
 CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
 CC optionally have phosphorothioate linkages which make them more resistant
 CC to degradation. The invention also relates to an oligonucleotide delivery
 CC complex comprising an oligonucleotide of the invention and a targeting
 CC agent, and a pharmaceutical composition comprising the oligonucleotide
 CC delivery complex. The oligonucleotides are able to induce either a cell-
 CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
 CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNN-3'
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g., macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergenic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic
 CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antitense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention

XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 20;
 Best Local Similarity 94.4%; Pred. No. 3.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGCTGTCAGGGGGG 18
 ||||| ||||| |||||
 DB 3 TCGTCGATGTCAGGGGGG 20

RESULT 10

AAS09631

ID AAS09631 standard; DNA; 20 BP.

XX AC AAS09631;

XX DT 26-SEP-2001 (first entry)

XX DE Immunoreactive CpG sequence-containing oligonucleotide #81.

XX CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antitense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.

XX OS Synthetic.

XX PN WO200151500-A1.

XX PD 19-JUL-2001.

XX PF 12-JAN-2001; 2001WO-US001122.

XX PR 14-JAN-2000; 2000US-0176115P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Klinman D, Ishii K, Verthelyi D;

XX WPI; 2001-442129/47.

XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.

XX Claim 5; Page 40; 46pp; English.

XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antitense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,

CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria
 XX
 SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 91.1%; Score 16.4; DB 4; Length 20;
 Best Local Similarity 94.4%; Pred. No. 3.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCCTCGGTCAGGGGGG 18
 ||||| ||||| ||||| |||||
 Db 3 TGCCTCGATGCAGGGGG 20
 ||||| ||||| ||||| |||||

RESULT 11
 AAS09590
 ID AAS09590 standard; DNA; 20 BP.
 XX
 AC AAS09590;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Immunoreactive CpG sequence-containing oligonucleotide #40.
 XX
 KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.
 XX
 OS Synthetic.
 XX
 PN WO200151500-A1.
 XX
 PD 19-JUL-2001.
 XX
 PF 12-JAN-2001; 2001WO-US001122.
 XX
 PR 14-JAN-2000; 2000US-0176115P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Kliman D, Ishii K, Verthelyi D;
 XX
 DR WPI; 2001-442129/47.
 XX
 PT Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.
 XX
 PS Claim 5; Page 33; 48pp; English.
 XX
 CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies

CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria
 XX
 SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 91.1%; Score 16.4; DB 4; Length 20;
 Best Local Similarity 94.4%; Pred. No. 3.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCCTCGGTCAGGGGGG 18
 ||||| ||||| ||||| |||||
 Db 3 TGCCTCGATGCAGGGGG 20
 ||||| ||||| ||||| |||||

RESULT 12
 AAS09632
 ID AAS09632 standard; DNA; 20 BP.
 XX
 AC AAS09632;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Immunoreactive CpG sequence-containing oligonucleotide #82.
 XX
 KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.
 XX
 OS Synthetic.
 XX
 PN WO200151500-A1.
 XX
 PD 19-JUL-2001.
 XX
 PF 12-JAN-2001; 2001WO-US001122.
 XX
 PR 14-JAN-2000; 2000US-0176115P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Kliman D, Ishii K, Verthelyi D;
 XX
 DR WPI; 2001-442129/47.
 XX
 PT Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.
 XX
 PS Claim 5; Page 40; 48pp; English.
 XX
 CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies

or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antiseptic therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines against hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, Anthrax and Listeria

CC the vaccine

XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

SQ Query Match 91.1%; Score 16.4; DB 4; Length 20;

Best Local Similarity 94.4%; Pred. No. 3.7e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCTCGGTGCAGGGGGG 18

Db 3 TGGCTCGGTGCAGGGGGG 20

RESULT 13

ABK46510

ID ABK46510 standard; DNA; 20 BP.

XX AC ABK46510;

XX DT 05-JUN-2002 (first entry)

XX DE Immunostimulatory unmethylated CpG oligodeoxynucleotide #100.

XX KW unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine;

XX KW Paramyxoviridae; F protein; respiratory syncytial virus; RSV;

XX KW viral bronchiolitis; pneumonia; infectious pulmonary disease;

XX KW bronchopulmonary dysplasia; congenital heart condition; ss.

XX OS Synthetic.

XX PN WO200211761-A2.

XX PD 14-FEB-2002.

XX PF 09-AUG-2001; 2001WO-US041633.

XX PR 10-AUG-2000; 2000US-0224011P.

XX PR 01-SEP-2000; 2000US-0229307P.

XX PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

XX PI Mond JJ, Prince G, Klinman DM;

XX DR WPI; 2002-227118/28.

XX PT Vaccine for immunizing patient against respiratory syncytial virus, has

PT epitopes of Paramyxoviridae F protein, and cytosine followed by guanine

PT linked by phosphate bond-oligodeoxynucleotides.

XX PS Claim 4; Page 9; 30pp; English.

XX CC The invention describes a vaccine comprising one or more epitopes of a

CC Paramyxoviridae F protein, and one or more CpG (cytosine followed by

CC guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The

CC vaccine is useful for vaccinating a patient especially against viruses of

CC the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the

CC primary cause of viral bronchiolitis and pneumonia in infants and

CC children, and infectious pulmonary disease in infants. RSV has been

CC particularly implicated in death of infants that are premature, have

CC bronchopulmonary dysplasia, or congenital heart conditions. This sequence

CC represents an oligodeoxynucleotide that can be used in the creation of

CC the vaccine

XX SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 6; Length 20;

Best Local Similarity 94.4%; Pred. No. 3.7e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCTCGGTGCAGGGGGG 18

Db 3 TGGCTCGGTGCAGGGGGG 20

RESULT 14

ABK46468

ID ABK46468 standard; DNA; 20 BP.

XX AC ABK46468;

XX DT 05-JUN-2002 (first entry)

XX DE Immunostimulatory unmethylated CpG oligodeoxynucleotide #58.

XX KW unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine;

XX KW Paramyxoviridae; F protein; respiratory syncytial virus; RSV;

XX KW viral bronchiolitis; pneumonia; infectious pulmonary disease;

XX KW bronchopulmonary dysplasia; congenital heart condition; ss.

XX OS Synthetic.

XX PN WO200211761-A2.

XX PD 14-FEB-2002.

XX PF 09-AUG-2001; 2001WO-US041633.

XX PR 10-AUG-2000; 2000US-0224011P.

XX PR 01-SEP-2000; 2000US-0229307P.

XX PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

XX PI Mond JJ, Prince G, Klinman DM;

XX DR WPI; 2002-227118/28.

XX PT Vaccine for immunizing patient against respiratory syncytial virus, has

PT epitopes of Paramyxoviridae F protein, and cytosine followed by guanine

PT linked by phosphate bond-oligodeoxynucleotides.

XX PS Claim 4; Page 8; 30pp; English.

XX CC The invention describes a vaccine comprising one or more epitopes of a

CC Paramyxoviridae F protein, and one or more CpG (cytosine followed by

CC guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The

CC vaccine is useful for vaccinating a patient especially against viruses of

CC the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the

CC primary cause of viral bronchiolitis and pneumonia in infants and

CC children, and infectious pulmonary disease in infants. RSV has been

CC particularly implicated in death of infants that are premature, have

CC bronchopulmonary dysplasia, or congenital heart conditions. This sequence

CC represents an oligodeoxynucleotide that can be used in the creation of

CC the vaccine

RESULT 15
ABK46509
ID ABK46509 standard; DNA; 20 BP.
XX
XX
AC ABK46509;
XX
DT 05-JUN-2002 (first entry)
XX
DE Immunostimulatory unmethylated CpG oligodeoxynucleotide #99.
XX
XX unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine;
KW Paramyxoviridae; F protein; respiratory syncytial virus; RSV;
KW viral bronchiolitis; pneumonia; infectious pulmonary disease;
KW bronchopulmonary dysplasia; congenital heart condition; ss.
XX
OS Synthetic.
XX
PN WO200211761-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US041633.
XX
PR 10-AUG-2000; 2000US-0224011P.
PR 01-SEP-2000; 2000US-0229307P.
XX
XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
PA
PI Mond JJ, Prince G, Kinnman DM;
XX
DR WPI; 2002-227118/28.
XX
XX
PT Vaccine for immunizing patient against respiratory syncytial virus, has
PT epitopes of Paramyxoviridae F protein, and cytosine followed by guanine
PT linked by phosphate bond-oligodeoxynucleotides.
XX
PS Claim 4; Page 9; 30pp; English.
XX
XX The invention describes a vaccine comprising one or more epitopes of a
CC Paramyxoviridae F protein, and one or more CpG (cytosine followed by
CC guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The
CC vaccine is useful for vaccinating a patient especially against viruses of
CC the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the
CC primary cause of viral bronchiolitis and pneumonia in infants and
CC children, and infectious pulmonary disease in infants. RSV has been
CC particularly implicated in death of infants that are premature, have
CC bronchopulmonary dysplasia, or congenital heart conditions. This sequence
CC represents an oligodeoxynucleotide that can be used in the creation of
CC the vaccine
XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TGGTCGGTGCAGGGGG 18
Db 3 TGGTCGATGCAGGGGG 20
Search completed: July 2, 2004, 08:31:39
Job time : 135.89 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:11:05 ; Search time 138.732 Seconds
(without alignments)
625.926 Million cell updates/sec

Title: US-10-068-160-19

Perfect score: 18
Sequence: 1 tgcacgcacgagggggg 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgm2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgm2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgm2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgm2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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- 13: /cgm2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 14: /cgm2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgm2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgm2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgm2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgm2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgm2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	15	US-10-068-160-19
2	18	100.0	20	13	Sequence 19, Appl
3	18	100.0	20	13	Sequence 498, App
4	18	100.0	20	13	Sequence 509, App
5	18	100.0	20	13	Sequence 542, App
6	18	100.0	20	15	US-09-874-991C-502
7	18	100.0	20	15	US-10-068-160-35
8	18	100.0	20	17	US-10-068-160-31
9	18	100.0	20	13	US-10-066-022-7
10	17	94.4	19	15	US-09-874-991C-519
11	16.4	91.1	18	13	US-09-874-991C-531
12	16.4	91.1	18	13	US-10-194-035-88
13	16.4	91.1	18	13	US-09-874-991C-503
14	16.4	91.1	18	13	US-09-874-991C-513
					Sequence 503, App
					Sequence 513, App
					Sequence 551, App
					Sequence 12, Appl

Sequence 14, Appl
Sequence 494, App
Sequence 502, App
Sequence 505, App
Sequence 512, App
Sequence 538, App
Sequence 550, App
Sequence 1, Appl
Sequence 31, Appl
Sequence 38, Appl
Sequence 54, Appl
Sequence 64, Appl
Sequence 32, Appl
Sequence 34, Appl
Sequence 37, Appl
Sequence 38, Appl
Sequence 39, Appl
Sequence 41, Appl
Sequence 43, Appl
Sequence 72, Appl
Sequence 1, Appl
Sequence 3, Appl
Sequence 176, App
Sequence 177, App
Sequence 500, App
Sequence 544, App
Sequence 524, App
Sequence 536, App
Sequence 515, App
Sequence 523, App

US-10-068-160-14
US-09-874-991C-494
US-09-874-991C-502
US-09-874-991C-505
US-09-874-991C-512
US-09-874-991C-538
US-09-874-991C-550
US-10-068-160-31
US-10-068-160-31
US-10-068-160-38
US-10-068-160-54
US-10-068-160-64
US-10-194-035-32
US-10-194-035-34
US-10-194-035-37
US-10-194-035-38
US-10-194-035-39
US-10-194-035-41
US-10-194-035-43
US-10-194-035-72
US-10-666-022-1
US-10-666-022-3
US-10-666-022-176
US-10-666-022-177
US-09-874-991C-500
US-09-874-991C-544
US-09-874-991C-524
US-09-874-991C-536
US-09-874-991C-515
US-09-874-991C-523

ALIGNMENTS

RESULT 1

US-10-068-160-19
Sequence 19, Application US/10068160
Publication No. US2003060440A1

GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, Dennis
APPLICANT: ISHII, Ken

APPLICANT: VERTHELYI, Daniela
TITLE OF INVENTION: OLIGONUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-61999
CURRENT FILING DATE: 2002-02-06
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patent version 3.1
SEQ ID NO 19

LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-10-068-160-19

Query Match 100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGAGGGGG 18

Db 1 TGCATCGACGACGAGGGGG 18

RESULT 2

US-09-874-991C-498

; Sequence 498, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 498
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-498

Query Match 100.0%; Score 18; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGAGGGGG 18
| | | | | | | | | | | | | | | | | |
Db 3 TGCATCGACGCGAGGGGG 20

RESULT 3

US-09-874-991C-509
; Sequence 509, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 509
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-509

Query Match 100.0%; Score 18; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGAGGGGG 18
| | | | | | | | | | | | | | | | | |
Db 3 TGCATCGACGCGAGGGGG 20

RESULT 4

US-09-874-991C-542
; Sequence 542, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES

; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 542
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-542

Query Match 100.0%; Score 18; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGAGGGGG 18
| | | | | | | | | | | | | | | | | |
Db 3 TGCATCGACGCGAGGGGG 20

RESULT 5

US-10-068-160-35
; Sequence 35, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, DENNIS
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-35

Query Match 100.0%; Score 18; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGAGGGGG 18
| | | | | | | | | | | | | | | | | |
Db 3 TGCATCGACGCGAGGGGG 20

RESULT 6

US-10-194-035-100
; Sequence 100, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, DENNIS
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12

; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-100

Query Match 100.0%; Score 18; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
|||
DB 3 TGCATCGACGCGGGGG 20

RESULT 7
US-10-666-022-7
; Sequence 7, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Kliman, Dennis M.
; APPLICANT: Vertelny, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; FILE REFERENCE: 4239-66999
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: misc_feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-7

Query Match 100.0%; Score 18; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
|||
DB 3 TGCATCGACGCGGGGG 20

RESULT 8
US-09-874-991C-519
; Sequence 519, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLIMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C

; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 820
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 519
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-519

Query Match 100.0%; Score 18; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
|||
DB 3 TGCATCGACGCGGGGG 20

RESULT 9
US-09-874-991C-531
; Sequence 531, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLIMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 531
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-531

Query Match 100.0%; Score 18; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
|||
DB 11 TGCATCGACGCGGGGG 28

RESULT 10
US-10-194-035-88
; Sequence 88, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLIMAN, DENNIS
; APPLICANT: VERHELTY, Daniela
; APPLICANT: ISHII, Ken
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14

; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-88

Query Match 94.4%; Score 17; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGG 17
DB 3 TGCATCGACGACGGGG 19

RESULT 11
US-09-874-991C-503
; Sequence 503, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 503
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-503

Query Match 91.1%; Score 16.4; DB 13; Length 18;
Best Local Similarity 94.4%; Pred. No. 77;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGG 18
DB 1 TGCATCGATCGACGGGG 18

RESULT 12
US-09-874-991C-513
; Sequence 513, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 513
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-513

Query Match 91.1%; Score 16.4; DB 13; Length 18;
Best Local Similarity 94.4%; Pred. No. 77;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGG 18
DB 1 TGCATCGATCGACGGGG 18

RESULT 13
US-09-874-991C-551
; Sequence 551, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 551
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-551

Query Match 91.1%; Score 16.4; DB 13; Length 18;
Best Local Similarity 94.4%; Pred. No. 77;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGG 18
DB 1 TGCATCGATCGACGGGG 18

RESULT 14
US-10-068-160-12
; Sequence 12, Application US/10068160
; Publication No. US2003006040A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-12

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Best Local Similarity 94.4%; Pred. No. 77;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 15

US-10-068-160-14
 ; Sequence 14, Application US/10068160
 ; Publication No. US2003006040A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
 ; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
 ; APPLICANT: KLIMAN, Dennis
 ; APPLICANT: ISHII, Ken
 ; APPLICANT: VERTHELYI, Daniela
 ; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
 ; FILE REFERENCE: 4239-61999
 ; CURRENT APPLICATION NUMBER: US/10/068,160
 ; CURRENT FILING DATE: 2002-02-05
 ; PRIOR APPLICATION NUMBER: 60/128,898
 ; PRIOR FILING DATE: 1999-04-12
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 ; OTHER INFORMATION: Oligonucleotide
 US-10-068-160-14

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 Db 1 TGCATCGATGCGAGGGGG 18
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Search completed: July 2, 2004, 13:58:26
 Job time : 138.732 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:36:05 ; Search time 633.732 Seconds
(without alignments)
1231.080 Million cell updates/sec

Title: US-10-068-160-20
Perfect score: 18
Sequence: 1 tcgctcggtgcagggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	17	94.4	19	6	AX194479	Sequence
2	17	94.4	19	6	AX465429	Sequence
3	16.4	91.1	20	6	AX194440	Sequence
4	16.4	91.1	20	6	AX194481	Sequence
5	16.4	91.1	20	6	AX194482	Sequence
6	16.4	91.1	20	6	AX465390	Sequence
7	16.4	91.1	20	6	AX465431	Sequence
8	16.4	91.1	20	6	AX465432	Sequence
9	16.4	91.1	10007	1	AE008951	Agrobacte
10	16.4	91.1	11009	1	AE007898	Continuation (23 o
11	16.4	91.1	110000	2	LMFLCHR32_22	Continuation (7 of
12	16.4	91.1	110000	2	LMFLCHR34_06	Continuation (7 of
13	16.4	91.1	178145	9	AC018659	Homo sapi
14	16.4	91.1	283100	1	SC0939110	Streptomy
15	16	88.9	1166	9	BC008984	Homo sapi
16	16	88.9	1182	9	AY286020	Homo sapi
17	16	88.9	1825	9	AY172561	Homo sapi
18	16	88.9	1851	9	AY286019	Homo sapi
19	16	88.9	134161	9	AC104336	Homo sapi
20	16	88.9	141567	2	AC133710	Oryza sat
21	16	88.9	143060	9	AL329472	Human DNA
22	16	88.9	160402	2	AC136491	Oryza sat
23	16	88.9	170908	2	AC022557	Homo sapi
24	16	88.9	190310	2	AC023225	Homo sapi
25	16	88.9	255952	2	AL513473	Homo sapi
26	16	88.9	302881	2	BX323850	Danio rer
27	15.4	85.6	19	6	AX194475	Sequence
28	15.4	85.6	19	6	AX194483	Sequence
29	15.4	85.6	19	6	AX465425	Sequence
30	15.4	85.6	19	6	AX465433	Sequence
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32	15.4	85.6	683	9	HSA333016	Homo sapi
33	15.4	85.6	701	9	HSA330295	Homo sapi
34	15.4	85.6	753	9	HSA338993	Homo sapi
35	15.4	85.6	765	6	AX438770	Sequence
36	15.4	85.6	771	9	HSA338994	Homo sapi
37	15.4	85.6	1392	6	AR387935	Sequence
38	15.4	85.6	1396	8	AX101989	Oryza sat
39	15.4	85.6	1716	9	HSU39195	Human clone
40	15.4	85.6	2722	8	AK100056	Oryza sat
41	15.4	85.6	2783	9	D50134	Homo sapien
42	15.4	85.6	2968	9	HSU52154	Human (G pro
43	15.4	85.6	10440	1	AE000800	Methanoba
44	15.4	85.6	10942	1	AE004107	Vibrio ch
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RESULT 1	AX194479	AX194479	19 bp	DNA	linear	PAT 28-AUG-2001
LOCUS	Sequence 79 from Patent WO0151500.					
DEFINITION	Sequence 79 from Patent WO0151500.					
ACCESSION	AX194479					
VERSION	AX194479.1	GI:15385135				
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM	artificial sequences.					
REFERENCE	1					
AUTHORS	Klinman,D., Ishii,K. and Verthelyi,D.					
TITLE	Oligodeoxynucleotide and its use to induce an immune response					
JOURNAL	Patent: WO 0151500-A 79 19-JUL-2001;					
	Secretary of the Department of Health and Human Services (US)					


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  Db 3 TCGTCGGTGCAGGGGG 19
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LOCUS      AX194440      19 bp      DNA      linear      PAT 16-JUL-2002
DEFINITION Sequence 97 from Patent WO0211761.
ACCESSION  AX194440
VERSION     AX194440.1 GI:21899792
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS    Mond, J.J., Prince, G. and Klimman, D.M.
TITLE      Vaccine against RSV.
JOURNAL    Patent: WO 0211761-A 97 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
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  Db 3 TCGTCGGTGCAGGGGG 19
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LOCUS      AX194440      20 bp      DNA      linear      PAT 28-AUG-2001
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ACCESSION  AX194440
VERSION     AX194440.1 GI:15385096
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS    Klimman, D., Ishii, K. and Vertehelyi, D.
TITLE      Oligodeoxynucleotide and its use to induce an immune response
JOURNAL    Patent: WO 0151500-A 40 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
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  Db 3 TCGTCGGTGCAGGGGG 20
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LOCUS      AX194481      20 bp      DNA      linear      PAT 28-AUG-2001
DEFINITION Sequence 81 from Patent WO0151500.
ACCESSION  AX194481
VERSION     AX194481.1 GI:15385137
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS    Klimman, D., Ishii, K. and Vertehelyi, D.
TITLE      Oligodeoxynucleotide and its use to induce an immune response
JOURNAL    Patent: WO 0151500-A 81 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
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  Db 3 TCGTCGGTGCAGGGGG 20
RESULT 5
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LOCUS      AX194482      20 bp      DNA      linear      PAT 28-AUG-2001
DEFINITION Sequence 82 from Patent WO0151500.
ACCESSION  AX194482
VERSION     AX194482.1 GI:15385138
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS    Klimman, D., Ishii, K. and Vertehelyi, D.
TITLE      Oligodeoxynucleotide and its use to induce an immune response
JOURNAL    Patent: WO 0151500-A 82 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
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DEFINITION Sequence 58 from Patent WO0211761.
ACCESSION AX465390
VERSION AX465390.1 GI:21899753
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Mond,J.J., Prince,G. and Klinman,D.M.
AUTHORS Vaccine against RSV
TITLE Patent: WO 0211761-A 58 14-FEB-2002;
JOURNAL HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 3 TCGTCGATGCAGGGGG 20
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LOCUS AX465431 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 99 from Patent WO0211761.
ACCESSION AX465431
VERSION AX465431.1 GI:21899794
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Mond,J.J., Prince,G. and Klinman,D.M.
AUTHORS Vaccine against RSV
TITLE Patent: WO 0211761-A 99 14-FEB-2002;
JOURNAL HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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Best Local Similarity 94.4%; Pred. No. 2.8e+03;
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Db 3 TCGTCGATGCAGGGGG 20
RESULT 8
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LOCUS AX465432 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 100 from Patent WO0211761.
ACCESSION AX465432
VERSION AX465432.1 GI:21899795
KEYWORDS

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SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mond,J.J., Prince,G. and Klinman,D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 100 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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Db 3 TCGTCGATGCAGGGGG 20
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DEFINITION Agrobacterium tumefaciens str. C58 At plasmid section 26 of 49 of
the complete sequence.
ACCESSION AE008951
VERSION AE008951.1 GI:17743725
KEYWORDS
SOURCE Agrobacterium tumefaciens str. C58 (U. Washington)
ORGANISM Agrobacterium tumefaciens str. C58 (U. Washington)
REFERENCE 1
AUTHORS Wood,D.W., Setubal,J.C., Kaul,R., Monks,D., Chen,L., Wood,G.E.,
Chen,Y., Woo,L., Kitajima,J.P., Okura,V.K., Almeida Jr.,N.F.,
Zhou,Y., Bovee Sr.,D., Chapman,P., Clendenning,J., Deatherage,G.,
Gillet,W., Grant,C., Guenther,D., Kutyavin,T., Levy,R., Li,M.,
McLelland,E., Palmieri,A., Raymond,C., Rouse,G.,
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Krespan,W., Perry,M., Gordon-Kamm,B., Liao,L., Kim,S., Hendrick,C.,
Zhao,Z., Dolan,M., Tingey,S.V., Tomb,J., Gordon,M.P., Olson,M.V.
and Nester,E.W.
TITLE The genome of the natural genetic engineer Agrobacterium
tumefaciens C58
JOURNAL Science 294 (5550), 2317-2323 (2001)
MEDLINE 21608550
PUBMED 11743193
REFERENCE 2
AUTHORS Wood,D.W., Setubal,J.C., Kaul,R., Monks,D., Chen,L., Wood,G.E.,
Chen,Y., Woo,L., Kitajima,J.P., Okura,V.K., Almeida Jr.,N.F.,
Zhou,Y., Bovee Sr.,D., Chapman,P., Clendenning,J., Deatherage,G.,
Gillet,W., Grant,C., Guenther,D., Kutyavin,T., Levy,R., Li,M.,
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Zhao,Z., Dolan,M., Tingey,S.V., Tomb,J., Gordon,M.P., Olson,M.V.
and Nester,E.W.
TITLE Direct Submission
JOURNAL Submitted (27-SEP-2001) Department of Microbiology, University of
Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA
98195-7242, USA
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RNPKSGDASVRIORAAPHVTVSFEKDLADLISIALPAQRMENDRSLDLLVNNAGI
MVPKSTQDFGELQGTNYLGHFALTALHPLLLKGTDAVVTVSVSVAARAKINF
ADINSKRYHPMRAYSQSLCLMFALBLQDRSRAAGVSSIAAHFVSVSTDLHNA
PGRNSLQALARTFLWFLPQVQAQALPFSATSKEVKSQGYGPDRLGETRGHPQA
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7411..8076
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/db_xref="GI:17743733"
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gene      8428..8847
CDS       8428..8847
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Query Match      91.1%; Score 16.4; DB 1; Length 10007;
Best Local Similarity 94.4%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1  TCGCTGCGTGCGAGGGGG 18
    |||||
DB 9276 TCGTTCGCTGCGAGGGGG 9293

RESULT 10
AE007898
LOCUS      AE007898      11009 bp      DNA      linear      BCT 18-DEC-2001
DEFINITION Agrobacterium tumefaciens str. C58 plasmid AT, section 26 of 50 of
            the complete sequence.
ACCESSION  AE007898 AE007872
VERSION     AE007898.1 GI:15162060
KEYWORDS
SOURCE      Agrobacterium tumefaciens str. C58 (Cereon)
ORGANISM    Agrobacterium tumefaciens str. C58 (Cereon)
            Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
            Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
REFERENCE   1 (bases 1 to 11009)
AUTHORS    Hinkle,G., Slater,S.C. and Goodner,B.
TITLE      Complete Genome Sequence of Agrobacterium tumefaciens C58
            (Rhizobium radiobacter C58), the Causative Agent of Crown Gall
            Disease in Plants
JOURNAL
REFERENCE   2 (bases 1 to 11009)
AUTHORS    Hinkle,G., Slater,S.C. and Goodner,B.
TITLE      Direct Submission
JOURNAL    Submitted (14-AUG-2001) Cereon Genomics, 45 Sidney Street,
            Cambridge, MA 02139, USA

FEATURES
source     1..11009
            /organism="Agrobacterium tumefaciens str. C58 (Cereon)"
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            /strain="C58"
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            /plasmid="At"
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            complement(73..1860)
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            Pseudomonas aeruginosa (strain PAO1)"
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            YDVLQSPQDYGTPDELKAFIDQAHGCHIMVLDDVYNHFGPAGNTLAAYAPAPK
            KHETPWGAPDZNAEVRSPFLQNAFTWLTSTYRFDGLRIDAADELAGDGEVFLIEM
            AREVKTRIRNHLVLTEDANNAASPTPMADGAILVDQWDDFFHVIHVAITNEEG
            GYEDPASRPYENURSLATGTFVYQGEPRSPNPAASGEPSGHLPHRPFVFLNHDQ
            AGNRLEPPLPPLPFTGLTEALLICQPTLVFMGDHGSANPPFPFSDPHDNR
            EQEIRNLKQAESQGBLPDASQWMDPNDQHTMQLSTLKTWHAETTEGROQRADWA
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NLQGOVQPLERAGMLGPHSLCTVDCLEVYDDMSFLKGLTTASAVTTVSPTVAREI
LTPMCMGMGVLAARRGDLRGIVNGVDHVNBPATDPYILLANETAATATRSINKYA
LLQALGLAPTQCFVGVSRILTQKGDILLPHVPLIIEKGRLLVGGSDTALEDSL
QALACRPELVCAHIGIDERLAHMIQAGSPFIQPSRPFPCGLTVALRYALPFIVS
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DLAA"
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/gene="AGR_PAT_414"
/note="hypothetical protein"
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/protein_id="AAK90664.1"
/db_xref="GI:15162065"
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regulator"
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/transl_table=11
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/db_xref="GI:15162066"
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DIASNAGISRRTPFPYPSKDEILLQSQIGEMLADAVRAPSSSTPIEVRDAI
GVCKVITPNDMIEMDRLMKTSFSVQAKQVSYVQQEGEYIYALSERWPFERSTALRY
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Gene

CDS

Gene

CDS

Gene

CDS

Gene

CDS

Gene

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      /transl_table=11
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      /db_xref="GI:15162070"
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CDS 10021..10929
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Best Local Similarity 94.4%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCCTCGGTGCAGGGGG 18
Db 9276 TGCCTCGGTGCAGGGGG 9293

RESULT 11
WPCOMMENT LMFLCHR32_22/c
Sequence split into 28 fragments LOCUS LMFLCHR32 Accession AL499622
Fragment Name Begin End
LMFLCHR32_00 1 110000
LMFLCHR32_01 100001 210000
LMFLCHR32_02 200001 310000
LMFLCHR32_03 300001 410000
LMFLCHR32_04 400001 510000
LMFLCHR32_05 500001 610000
LMFLCHR32_06 600001 710000
LMFLCHR32_07 700001 810000
LMFLCHR32_08 800001 910000
LMFLCHR32_09 900001 1010000
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LMFLCHR32_11 1100001 1210000
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LMFLCHR32_25 2500001 2610000
LMFLCHR32_26 2600001 2710000
LMFLCHR32_27 2700001 2727709

Continuation (23 of 28) of LMFLCHR32 from base 2200001 (AL499622 Leishmania major chro

Query Match 91.1%; Score 16.4; DB 2; Length 110000;
Best Local Similarity 94.4%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCCTCGGTGCAGGGGG 18
Db 23220 TGCCTCGGTGCAGGGGG 23203

RESULT 12
WPCOMMENT LMFLCHR34_06
Sequence split into 18 fragments LOCUS LMFLCHR34 Accession AL499623
Fragment Name Begin End
LMFLCHR34_00 1 110000
LMFLCHR34_01 100001 210000
LMFLCHR34_02 200001 310000
LMFLCHR34_03 300001 410000
LMFLCHR34_04 400001 510000
LMFLCHR34_05 500001 610000
LMFLCHR34_06 600001 710000
LMFLCHR34_07 700001 810000
LMFLCHR34_08 800001 910000
LMFLCHR34_09 900001 1010000
LMFLCHR34_10 1000001 1110000
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Unpublished
2 (bases 1 to 178145)
Worley, K.C.
Direct Submission
Submitted (16-DEC-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 178145)
Worley, K.C.
Direct Submission
Submitted (01-JUN-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 178145)
Worley, K.C.
Direct Submission
Submitted (05-JUN-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 178145)
Worley, K.C.
Direct Submission
Submitted (31-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
6 (bases 1 to 178145)
Worley, K.C.
Direct Submission
Submitted (18-MAR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jun 1, 2001 this sequence version replaced gi.14269664.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL:
<http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.
Location/Qualifiers
1. 178145
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6933..7081
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8003..8036
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8243..8568
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10495..10529
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Query Match          91.1%; Score 16.4; DB 9; Length 178145;
Best Local Similarity 94.4%; Pred. No. 8.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  TCGCTCGGTGTCAGGGGGG 18
      ||||| ||||| |||||
DB      94986 TCGCTCGGTGTCAGGGGGG 94969

RESULT 14
LOCUS   SC0939110                283100 bp    DNA        linear    BCT 11-FEB-2003
DEFINITION Streptomyces coelicolor A3(2) complete genome; segment 77/9.
ACCESSION AL939110 AL035591 AL079332 AL096811 AL096844 AL096844
VERSION   AL096849 AL109848 AL132644 AL445403 AL513407 AL591322 AL645882
KEYWORDS  AL939110.1 GI:24413753
SOURCE    Streptomyces coelicolor A3(2)
ORGANISM  Streptomyces coelicolor A3(2)
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE
AUTHORS   Bentley,S.D., Chater,K.F., Cerdeno-Tarraga,A.M., Challis,G.L.,
          Thomson,N.R., James,K.D., Harris,D.E., Quail,M.A., Kieser,H.,
          Harper,D., Bateman,A., Brown,S., Chandra,G., Chen,C.W., Collins,M.,
          Cronin,A., Fraser,A., Goble,A., Hidalgo,J., Hornsby,T., Howarth,S.,
          Huang,C.H., Kieser,T., Larke,L., Murphy,L., Oliver,K., O'Neill,S.,
          Rabinowitz,E., Rajandream,M.A., Rutherford,K., Rutter,S.,
          Seeger,K., Saunders,D., Sharp,S., Squares,R., Squares,S.,
          Taylor,K., Warren,T., Wietzorrek,A., Woodward,J., Barrall,B.G.,
          Parkhill,J. and Hopwood,D.A.
          Complete genome sequence of the model actinomycete Streptomyces
          coelicolor A3(2)
          Nature 417 (6885), 141-147 (2002)
JOURNAL   NATURE
MEDLINE   21996410
PUBMED    12000953
REFERENCE 2 (bases 1 to 283100)
AUTHORS   Bentley,S.D.
TITLE     Direct Submission
JOURNAL   Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces
          Sequencing team, Sanger Institute, Wellcome Trust Genome Campus,
          Hinxton, Cambridge CB10 1SA E-mail: sds@sanger.ac.uk
          On or before Oct 26, 2002 this sequence version replaced
          GI:20520819, gi:20520879, gi:20520880, gi:20520919, gi:20520821,
          gi:20520887, gi:20520888, gi:20520889, gi:20520918,
          gi:20520915, gi:20520918,
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              /strain="A3(2)"
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                  /note="SC130A.19, unknown, len: 153 aa; similar to many of
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                  hypothetical protein from Mycobacterium tuberculosis (151
                  aa) fasta scores; opt: 639, z-score: 785.9, E(): 0. (60.8%
                  identity in 148 aa overlap) and SW:NODN RHILY modulation
                  protein from Rhizobium leguminosarum (161 aa) fasta
                  scores; opt: 388, z-score: 482.2, E(): 1.6e-19, (44.8%
                  identity in 145 aa overlap)"
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Search completed: July 2, 2004, 10:08:13
Job time : 636.732 secs

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RESULT 15
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LOCUS Homo sapiens, hypothetical protein FLJ23476, clone MGC:16780
DEFINITION IMAGE:4338853, mRNA, complete cds.
ACCESSION BC008984
VERSION BC008984.1 GI:14290439
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1166)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (30-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgaps@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villalob@bcm.tmc.edu
Villalob, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 12 Row: 0 Column: 18
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 10440178.

FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:16780 IMAGE:4338853"
/tissue_type="Lymph, lymphoma"
/clone_lib="NIH_MGC_85"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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ORIGIN
Query Match 88.9%; Score 16; DB 9; Length 1166;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCCTCGGTGCAGGGGG 17
Db 52 GCCTCGGTGCAGGGGG 67

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:09:30 ; Search time 28.2073 Seconds
(without alignments)
354.132 Million cell updates/sec

Title: US-10-068-160-19

Perfect score: 18
Sequence: 1 tgcacgcagcagggggg 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.8	82.2	107	3	US-09-193-068-21
2	14.8	82.2	1443	4	US-09-537-168-1
3	14.8	82.2	1683	3	US-08-814-052-5
4	14.8	82.2	1683	3	US-08-812-829-5
5	14.8	82.2	1777	1	US-08-146-422-33
6	14.8	82.2	1777	1	US-08-253-575-1
7	14.8	82.2	1777	1	US-08-626-554-16
8	14.8	82.2	1893	3	US-08-814-052-7
9	14.8	82.2	1893	3	US-08-812-829-7
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11	14.8	82.2	1920	1	US-08-720-899-1
12	14.8	82.2	1920	1	US-08-459-610-1
13	14.8	82.2	1920	2	US-08-343-804-1
14	14.8	82.2	1920	2	US-08-687-399-1
15	14.8	82.2	1920	2	US-08-600-908A-1
16	14.8	82.2	1920	3	US-08-683-838A-1
17	14.8	82.2	1920	3	US-09-182-859-1
18	14.8	82.2	1920	3	US-09-170-670-12
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21	14.8	82.2	1920	4	US-09-537-168-3
22	14.8	82.2	1920	4	US-09-672-459-1
23	14.8	82.2	1920	4	US-09-636-252A-1
24	14.8	82.2	1920	4	US-09-545-586-12
25	14.8	82.2	1920	4	US-10-186-042-1
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27	14.8	82.2	1926	3	US-09-183-412-12

28 14.8 82.2 1968 1 US-08-468-700-33 Sequence 33, Appl
29 14.8 82.2 1968 1 US-08-645-971-1 Sequence 1, Appl
30 14.8 82.2 1968 1 US-08-468-220-31 Sequence 31, Appl
31 14.8 82.2 1968 2 US-08-468-698-31 Sequence 31, Appl
32 14.8 82.2 1968 2 US-08-704-706A-33 Sequence 33, Appl
33 14.8 82.2 1968 3 US-08-890-383-1 Sequence 1, Appl
34 14.8 82.2 1968 3 US-08-914-679A-1 Sequence 1, Appl
35 14.8 82.2 1968 3 US-08-985-659-33 Sequence 33, Appl
36 14.8 82.2 1968 3 US-08-194-684A-31 Sequence 31, Appl
37 14.8 82.2 1968 5 PCT-US95-10426-31 Sequence 31, Appl
38 14.8 82.2 1968 5 PCT-US95-10426-31 Sequence 31, Appl
39 14.8 82.2 2149 1 US-07-623-953-2 Sequence 2, Appl
40 14.8 82.2 2253 3 US-08-814-052-1 Sequence 1, Appl
41 14.8 82.2 2253 1 US-08-812-829-1 Sequence 1, Appl
42 14.8 82.2 5677 1 US-07-623-953-4 Sequence 4, Appl
43 14.4 80.0 215 3 US-08-751-359-23 Sequence 23, Appl
44 14.4 80.0 215 4 US-08-907-146-23 Sequence 23, Appl
45 14.4 80.0 484 4 US-09-221-017B-181 Sequence 181, App

ALIGNMENTS

RESULT 1
US-09-193-068-21
; Sequence 21, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjulf, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 107
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; OTHER INFORMATION: n = a, c, g, t
US-09-193-068-21

Query Match 82.2%; Score 14.8; DB 3; Length 107;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGGG 18
Db 9 TGCATCGACACAGGGAGG 26

RESULT 2
US-09-537-168-1
; Sequence 1, Application US/09537168
; Patent No. 6410295
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/09/537,168
; CURRENT FILING DATE: 2000-03-29
; EARLIER APPLICATION NUMBER: PA 1999 00437
; EARLIER FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: 60/127,427

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; EARLIER FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Bacillus amyloliquefaciens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1443)
US-09-537-168-1

Query Match      82.2%; Score 14.8; DB 4; Length 1443;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGGG 18
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Db 876 TGCATCGACGACGGGGG 893

RESULT 3
US-08-814-052-5
; Sequence 5, Application US/08814052
; Patent No. 6015783
; GENERAL INFORMATION:
; APPLICANT: von der Osten, Claus
; APPLICANT: Cherry, Joel R.
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Vind, Jesper
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: PROCESS FOR REMOVAL OR BLEACHING OF SOILING
; TITLE OF INVENTION: OR STAINS FROM CELLULOSIC FABRIC
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 60157830 No. 6015783disk of No. 6015783th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 06-MAR-1997
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4684.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1683 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-814-052-5

Query Match      82.2%; Score 14.8; DB 3; Length 1683;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGGG 18
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Db 876 TGCATCGACGACGGGGG 893

RESULT 5
US-08-146-422-33
; Sequence 33, Application US/08146422
; Patent No. 5543576
; GENERAL INFORMATION:
; APPLICANT: VAN COIJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KEIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; APPLICANT: QUAX, WILHEMUS J.
; TITLE OF INVENTION: PRODUCTION OF ENZYMES IN SEEDS AND THEIR
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 60177510 No. 6017751disk of No. 6017751th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 06-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4690.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1683 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-812-829-5

Query Match      82.2%; Score 14.8; DB 3; Length 1683;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGGG 18
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Db 969 TGCATCGACGACGGGGG 986

RESULT 5
US-08-146-422-33
; Sequence 33, Application US/08146422
; Patent No. 5543576
; GENERAL INFORMATION:
; APPLICANT: VAN COIJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KEIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; APPLICANT: QUAX, WILHEMUS J.
; TITLE OF INVENTION: PRODUCTION OF ENZYMES IN SEEDS AND THEIR
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/146,422
APPLICATION NUMBER: 514
FILING DATE: 02-NOV-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KENNEDY, BILL
REGISTRATION NUMBER: 33,407
REFERENCE/DOCKET NUMBER: 44615-20011.23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1777 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-146-422-33

Query Match 82.2%; Score 14.8; DB 1; Length 1777;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCATCGACGAGGGGGG 18
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Db 978 TGCATCGACGAGGGG 995

RESULT 6
US-08-253-575-1
Sequence 1, Application US/08253575
Patent No. 5705375
GENERAL INFORMATION:
APPLICANT: VAN COVEN, ALBERT J.J.
APPLICANT: RIETVELD, KRJUN
APPLICANT: QUAX, WILHELMUS J.
APPLICANT: VAN DEN ELZEN, PETRUS J.M.
APPLICANT: PEN, JAN
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: SIJMONS, PETER C.
TITLE OF INVENTION: TRANSGENIC PLANTS HAVING A MODIFIED
TITLE OF INVENTION: CARBOHYDRATE CONTENT
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,575
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/849,422

FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20033.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1777 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-253-575-1

Query Match 82.2%; Score 14.8; DB 1; Length 1777;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCATCGACGAGGGGGG 18
|||||
Db 978 TGCATCGACGAGGGG 995

RESULT 7
US-08-626-554-16
Sequence 16, Application US/08626554
Patent No. 5714474
GENERAL INFORMATION:
APPLICANT: VAN OOLJEN, ALBERT J.J.
APPLICANT: RIETVELD, KRJUN
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: PEN, JAN
APPLICANT: SIJMONS, PETER C.
APPLICANT: VERWOERD, TRUNIS C.
APPLICANT: QUAX, WILHELMUS J.
TITLE OF INVENTION: PRODUCTION OF ENZYMES IN SEEDS AND THEIR
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE NW
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,554
FILING DATE: 02-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 26192-20011.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030 MESNFOERSWSH
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1777 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-626-554-16

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Query Match      82.2%; Score 14.8; DB 1; Length 1777;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGAGGGGG 18
    |||||
Db 978 TGCATCGACACAGGAGG 995

RESULT 8
US-08-814-052-7
; Sequence 7, Application US/08814052
; Patent No. 6015783
; GENERAL INFORMATION:
; APPLICANT: von der Osten, Claus
; APPLICANT: Cherry, Joel R.
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Vind, Jesper
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: PROCESS FOR REMOVAL OR BLEACHING OF SOILING
; OR STAINS FROM CELLULOSIC FABRIC
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6015783 No. 6015783disk of No. 6015783th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,052
; FILING DATE: 06-MAR-1997
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4684.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1893 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-814-052-7

Query Match      82.2%; Score 14.8; DB 3; Length 1893;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGAGGGGG 18
    |||||
Db 1323 TGCATCGACACAGGAGG 1340

RESULT 9
US-08-812-829-7
; Sequence 7, Application US/08812829
; Patent No. 6017751
; GENERAL INFORMATION:
; APPLICANT: von der Osten, Claus
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Vind, Jesper
; APPLICANT: Rasmussen, Michael Dolberg
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; TITLE OF INVENTION: PROCESS FOR REMOVAL OR BLEACHING OF SOILING
; OR STAINS FROM CELLULOSIC FABRIC
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6017751 No. 6017751disk of No. 6017751th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,829
; FILING DATE: 06-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4690.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1893 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-812-829-7

Query Match      82.2%; Score 14.8; DB 3; Length 1893;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGAGGGGG 18
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Db 1323 TGCATCGACACAGGAGG 1340

RESULT 10
US-09-264-097-1
; Sequence 1, Application US/09264097
; Patent No. 6287826
; GENERAL INFORMATION:
; APPLICANT: No. 6287826man, Barrie Edmund
; APPLICANT: Hendriksen, Hanne Vang
; TITLE OF INVENTION: Enzymatic Preparation of Glucose Syrup
; FROM STARCH
; FILE REFERENCE: 5278.200-US
; CURRENT APPLICATION NUMBER: US/09/264,097
; CURRENT FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: PA 0321/98
; EARLIER FILING DATE: 1998-03-09
; EARLIER APPLICATION NUMBER: 60/079,209
; EARLIER FILING DATE: 1998-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1912
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (421)...(1872)
; NAME/KEY: mat peptide
; LOCATION: (421)...(1869)
US-09-264-097-1
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Query Match 82.2%; Score 14.8; DB 3; Length 1918;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGGG 18
|||||
Db 1302 TGCATCGACGACGGGAGG 1319

RESULT 11

US-08-720-899-1
; Sequence 1, Application US/08720899
; Patent No. 5753460
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5753460 No. 5753460th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08720,899
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1920 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 334..1872
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 334..420
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 421..1869
US-08-720-899-1

Query Match 82.2%; Score 14.8; DB 1; Length 1920;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGGG 18
|||||
Db 1302 TGCATCGACGACGGGAGG 1319

RESULT 12

US-08-459-610-1
; Sequence 1, Application US/08459610
; Patent No. 5801043
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5801043 No. 5801043th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,610
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1920 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 334..1872
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 334..420
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 421..1869
US-08-459-610-1

Query Match 82.2%; Score 14.8; DB 1; Length 1920;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGGG 18
|||||
Db 1302 TGCATCGACGACGGGAGG 1319

RESULT 13

US-08-343-804-1
; Sequence 1, Application US/08343804
; Patent No. 5830837
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan

APPLICANT: Thellersen, Marianne
 TITLE OF INVENTION: AMYLASE VARIANTS
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 58308370 No. 5830837disk of No. 5830837th America, Inc.
 STREET: 405 Lexington Avenue, 64th Floor
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10174-6401

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/343,804
 FILING DATE: 22-NOV-1994
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Lowney Dr., Karen A.
 REGISTRATION NUMBER: 31,274
 REFERENCE/DOCKET NUMBER: 4054.214-US
 TELEPHONE: 212-867-0123
 TELEFAX: 212-867-0123

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1920 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

FEATURE:
 NAME/KEY: CDS
 LOCATION: 334..1872
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 334..420
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 421..1869
 US-08-343-804-1

Query Match 82.2%; Score 14.8; DB 2; Length 1920;
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCATCGACGACGAGGGG 18
 Db 1302 TGCATCGACGACGAGG 1319

RESULT 14
 US-08-687-399-1
 Sequence 1, Application US/08687399
 Patent No. 5928381
 GENERAL INFORMATION:
 APPLICANT: Toft, Annette H.
 APPLICANT: Marcher, Dorte
 APPLICANT: Pedersen, Hanne H.
 APPLICANT: Nilsson, Thomas E.
 TITLE OF INVENTION: A Combined Desizing and Bleaching
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 59283810 No. 5928381disk of No. 5928381th America, Inc.
 STREET: 405 Lexington Avenue, 64th Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6401
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/687,399
 FILING DATE:
 CLASSIFICATION: 008

ATTORNEY/AGENT INFORMATION:
 NAME: Lambiris, Elias J.
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 4127.204-US
 TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1920 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

FEATURE:
 NAME/KEY: CDS
 LOCATION: 334..1869
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 334..420
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 421..1869
 US-08-687-399-1

Query Match 82.2%; Score 14.8; DB 2; Length 1920;
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCATCGACGACGAGGGG 18
 Db 1302 TGCATCGACGACGAGG 1319

RESULT 15
 US-08-600-908A-1
 Sequence 1, Application US/08600908A
 Patent No. 5989169
 GENERAL INFORMATION:
 APPLICANT: Svendsen, Allan
 APPLICANT: Bisg rd-Frantzen, Henrik
 APPLICANT: Borchert, Torben Vedel
 TITLE OF INVENTION: '-Amylase Mutants
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 5989169o No. 5989169disk of No. 5989169th America, Inc.
 STREET: 405 Lexington Avenue, 64th Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/600,908A
 FILING DATE: 13-FEB-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Green, Reza
 REGISTRATION NUMBER: 38,475
 REFERENCE/DOCKET NUMBER: 4394.204-US
 TELECOMMUNICATION INFORMATION:

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;
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1920 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
; NAME/KEY: CDS
; LOCATION: 334..1869
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 334..420
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 421..1869
;
US-08-600-908A-1

Query Match      82.2%; Score 14.8; DB 2; Length 1920;
Best Local Similarity 88.9%; Pred.No. 1.1e+02;
Matches 16; Conservatives 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 TGCATCGACGACGAGGGGG 18
        |||||
Db      1302 TGCATCGACGACGAGGG 1319

Search completed: July 2, 2004, 13:37:53
Job time : 29.2073 secs
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 06:05:50 ; Search time 134.89 Seconds

(without alignments)
566.887 Million cell updates/sec

Title: US-10-068-160-19

Perfect score: 18
Sequence: 1 tgcacgacgcagggggg 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001a2:*
5: Geneseqn2001b2:*
6: Geneseqn2002s:*
7: Geneseqn2003a2:*
8: Geneseqn2003b2:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	20	4	AAS09650 Immunorea
2	18	100.0	20	6	ABL35616 Immunosti
3	18	100.0	20	6	ABL35572 Immunosti
4	18	100.0	20	6	ABL35583 Immunosti
5	18	100.0	20	7	Acc48314 Cpg oligo
6	18	100.0	20	7	Acc48304 Cpg oligo
7	18	100.0	20	8	Acc83119 D class C
8	18	100.0	20	9	ADD01057 Cpg D oli
9	18	100.0	28	6	ABL35605 Immunosti
10	18	100.0	28	6	ABL35593 Immunosti
11	17	94.4	19	4	AAC80668 Immunogen
12	17	94.4	19	4	AAS09638 Immunorea
13	17	94.4	19	6	ABK46516 Immunorea
14	16.4	91.1	18	6	ABL35577 Immunosti
15	16.4	91.1	18	6	ABL35587 Immunosti
16	16.4	91.1	18	6	ABL35625 Immunosti
17	16.4	91.1	18	9	ADD01052 Cpg D oli
18	16.4	91.1	20	4	AAC80619 Immunogen
19	16.4	91.1	20	4	AAC80621 Immunogen
20	16.4	91.1	20	4	AAC80652 Immunogen
21	16.4	91.1	20	4	AAC80614 Immunogen
22	16.4	91.1	20	4	AAC80612 Immunogen
23	16.4	91.1	20	4	AAC80617 Immunogen

24	16.4	91.1	20	4	AAC80618 Immunogen
25	16.4	91.1	20	4	AAC80623 Immunogen
26	16.4	91.1	20	4	AAS09622 Immunorea
27	16.4	91.1	20	4	AAS09591 Immunorea
28	16.4	91.1	20	4	AAS09582 Immunorea
29	16.4	91.1	20	4	AAS09587 Immunorea
30	16.4	91.1	20	4	AAS09589 Immunorea
31	16.4	91.1	20	4	AAS09593 Immunorea
32	16.4	91.1	20	4	AAS09584 Immunorea
33	16.4	91.1	20	4	AAS09588 Immunorea
34	16.4	91.1	20	6	ABL35576 Immunosti
35	16.4	91.1	20	6	ABL35586 Immunosti
36	16.4	91.1	20	6	ABL35568 Immunosti
37	16.4	91.1	20	6	ABL35624 Immunosti
38	16.4	91.1	20	6	ABL35579 Immunosti
39	16.4	91.1	20	6	ABL35620 Immunosti
40	16.4	91.1	20	6	ABL35612 Immunosti
41	16.4	91.1	20	6	ABK46500 Immunosti
42	16.4	91.1	20	6	ABK46469 Immunosti
43	16.4	91.1	20	6	ABK46460 Immunosti
44	16.4	91.1	20	6	ABK46465 Immunosti
45	16.4	91.1	20	6	ABK46471 Immunosti

ALIGNMENTS

RESULT 1

AAS09650

ID AAS09650 standard; DNA; 20 BP.

XX AAS09650;

XX AAS09650;

DT 26-SEP-2001 (first entry)

XX Immunoreactive Cpg sequence-containing oligonucleotide #100.

XX Cpg sequence; immune response; non-B cell activation; interferon gamma;

KW IFN-gamma; humoral; antibody production; interleukin-6 production;

KW therapeutic; allergy; anthrax; cancer; autoimmune disorder; infection;

KW bio-warfare; vaccine; antitense therapy; eczema; allergic rhinitis;

KW corvax; hay fever; urticaria; hives; food allergy; atopic condition;

KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;

KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;

KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;

KW Leishmania; Ebola; Anthrax; Listeria; ss.

XX Synthetic.

OS WO200151500-A1.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-US001122.

XX 14-JAN-2000; 2000US-0176115P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Klinman D, Iehii K, Verthelyi D;

XX WPI; 2001-442129/47.

Oligodeoxynucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple Cpg sequences.

Claim 5; Page 43; 48pp; English.

AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10 nucleotides comprising multiple Cpg sequences, where one of the Cpg sequences is different from another of the multiple Cpg sequences. The

CC ODN are useful for inducing an immune response, preferably a cell-mediated immune response, involving non-B cell activation, interferon gamma (IFN-gamma) production or a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma, cancer, e.g. solid tumour cancer, a disease associated with the immune system e.g. autoimmune disorder or an immune system deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antisense therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines against hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, CC Anthrax and Listeria

SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
Db 3 TGCATCGACGCGGGGG 20

RESULT 2

ABL35616
ID ABL35616 standard; DNA; 20 BP.

AC ABL35616;

XX 04-APR-2002 (first entry)

XX Immunostimulatory oligonucleotide SEQ ID NO: 542.

XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine; infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.

OS Synthetic.

XX Key Location/Qualifiers

FT misc_RNA

FT 1..20

FT /tag= a

FT /note= "optionally thymidine is replaced by uracil to form RNA or DNA/RNA hybrids. Thymidine is linked to at least one other base through a ribose sugar"

XX W0200193902-A2.

XX 13-DEC-2001.

XX 07-JUN-2001; 2001WO-US018276.

XX 07-JUN-2000; 2000US-0209797P.

XX (BIOS-) BIOSYNEXUS INC.

XX Mond JJ, Flora M, Klinman DM;

XX WPI; 2002-130570/17.

XX New immunostimulatory compositions comprising RNA/DNA hybrid oligonucleotides, useful for enhancing an immune response or inducing

PT cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.

XX Example 11; Page 62; 68pp; English.

XX The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a bio-warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention

SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
Db 3 TGCATCGACGCGGGGG 20

RESULT 3

ABL35572

ID ABL35572 standard; DNA; 20 BP.

XX ABL35572;

XX 04-APR-2002 (first entry)

XX Immunostimulatory oligonucleotide SEQ ID NO: 498.

XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine; infection; allergy; cancer; hypersensitivity; bio-warfare; immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV; immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.

OS Synthetic.

XX Key Location/Qualifiers

FT misc_RNA

FT 1..20

FT /tag= a

FT /note= "optionally thymidine is replaced by uracil to form RNA or DNA/RNA hybrids. Thymidine is linked to at least one other base through a ribose sugar"

XX W0200193902-A2.

XX 13-DEC-2001.

XX 07-JUN-2001; 2001WO-US018276.

XX 07-JUN-2000; 2000US-0209797P.

XX (BIOS-) BIOSYNEXUS INC.

XX Mond JJ, Flora M, Klinman DM;

XX WPI; 2002-130570/17.

XX New immunostimulatory compositions comprising RNA/DNA hybrid oligonucleotides, useful for enhancing an immune response or inducing

PT cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.

XX PS Example 11; Page 61; 68pp; English.

XX CC The present invention relates to an immunostimulatory composition, which

CC comprises at least one oligonucleotide comprising both an RNA region and

CC a DNA region. The composition is useful for enhancing an immune response

CC or inducing cytokines. It can be used as a vaccine adjuvant and in

CC treating diseases, including pathogenic infection, (non-)malignant

CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or

CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies

CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,

CC hepatitis, HIV or malaria. The composition is also useful for treating,

CC preventing or ameliorating the symptoms resulting from exposure to a bio-

CC warfare agent, e.g. Ebola, Anthrax or listeria. The present sequence is

CC an immunostimulatory oligonucleotide described in the exemplification of

CC the invention

XX SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGAGGGGG 18

Db 3 TGCATCGACGCGAGGGGG 20

RESULT 4

ABL35583

ID ABL35583 standard; DNA; 20 BP.

XX AC ABL35583;

XX DT 04-APR-2002 (first entry)

XX DE Immunostimulatory oligonucleotide SEQ ID NO: 509.

XX KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;

XX KW infection; allergy; cancer; hypersensitivity; bio-warfare;

XX KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;

XX KW immunosuppressive; protooncogene; virucide; hepatotropic; gene therapy;

XX KW antiinflammatory; antibacterial; ss.

XX OS Synthetic.

XX EH Key

XX FT misc_RNA

XX FT 1..20

XX FT /tag= a

XX FT /note= "optionally thymidine is replaced by uracil to

XX FT form RNA or DNA/RNA hybrids. Thymidine is linked to at

XX FT least one other base through a ribose sugar"

XX PN WO200193902-A2.

XX PD 13-DEC-2001.

XX PF 07-JUN-2001; 2001WO-US018276.

XX PR 07-JUN-2000; 2000US-0209797P.

XX PA (BIOS-) BIOSYNEXUS INC.

XX PI Mond JJ, Flora M, Klinman DM;

XX DR WPI; 2002-130570/17.

XX CC New immunostimulatory compositions comprising RNA/DNA hybrid

PT oligonucleotides, useful for enhancing an immune response or inducing

PT cytokines, particularly for treating diseases, e.g. cancer, allergy or

PT HIV infection.

XX PS Example 11; Page 61; 68pp; English.

XX CC The present invention relates to an immunostimulatory composition, which

CC comprises at least one oligonucleotide comprising both an RNA region and

CC a DNA region. The composition is useful for enhancing an immune response

CC or inducing cytokines. It can be used as a vaccine adjuvant and in

CC treating diseases, including pathogenic infection, (non-)malignant

CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or

CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies

CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,

CC hepatitis, HIV or malaria. The composition is also useful for treating,

CC preventing or ameliorating the symptoms resulting from exposure to a bio-

CC warfare agent, e.g. Ebola, Anthrax or listeria. The present sequence is

CC an immunostimulatory oligonucleotide described in the exemplification of

CC the invention

XX SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGAGGGGG 18

Db 3 TGCATCGACGCGAGGGGG 20

RESULT 5

ACC48314

ID ACC48314 standard; DNA; 20 BP.

XX AC ACC48314;

XX DT 11-AUG-2003 (first entry)

XX DE CpG oligodeoxynucleotide DV30.

XX KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;

XX KW cytostatic; immunostimulant; gene therapy; ss.

XX OS Synthetic.

XX PN WO2003020894-A2.

XX PD 13-MAR-2003.

XX PF 13-AUG-2002; 2002WO-US025732.

XX PR 14-AUG-2001; 2001US-0312190P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Klinman DM, Gursel M, Verthelyi D;

XX DR WPI; 2003-300874/29.

XX CC Generating mature dendritic cells for tumor immunotherapy or as vaccines

PT for activating the immune system to treat diseases such as cancer,

PT comprises contacting a dendritic cell precursor with a D type

PT oligodeoxynucleotide.

XX PS Disclosure; Fig 8; 69pp; English.

XX CC The present sequence is that of CpG oligodeoxynucleotide DV30 of the

CC invention. A claimed method for generating dendritic cells involves

CC contacting a dendritic cell precursor, especially a monocyte, with a D

CC type oligodeoxynucleotide (see ACC48294) containing a central

CC unethylyated CpG motif. The method is useful for generating mature

CC dendritic cells and enhancing T cell responses, thus enhancing antigen

CC presentation. Mature dendritic cells are useful for tumour immunotherapy,

CC for augmenting an immune response to an infectious agent or to a vaccine,

CC and as vaccines to prevent future infection or to activate the immune

CC system to treat diseases such as cancer. Mature dendritic cells may also

CC be used to produce activated T lymphocytes

QY 1 TGCATCGACGCGGGGG 18
 |||||
 Db 3 TGCATCGACGCGGGGG 20

RESULT 8
 ADD01057
 ID ADD01057 standard; DNA; 20 BP.
 XX
 AC ADD01057;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE CpG D oligonucleotide SEQ ID NO:21.
 XX
 KW vascular endothelial growth factor; VEGF; CpG oligonucleotide;
 KW neovascularisation; angiogenesis; vulnerary; vasotropic;
 KW antiarteriosclerotic; gene therapy; skin graft; male pattern baldness;
 KW atherosclerosis; ischaemia; ss.
 XX
 OS Synthetic.
 XX
 PN WO2003054161-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 19-DEC-2002; 2002WO-US040955.
 XX
 PR 20-DEC-2001; 2001US-0343457P.
 XX
 PA (UYTE-) UNIV TENNESSEE RES CORP.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Klinman DM, Zheng M, Rouse BT;
 XX
 DR WPI; 2003-559138/52.
 XX
 PT Inducing the production of vascular endothelial growth factor by a cell,
 PT useful for inducing angiogenesis, comprises contacting the cell with a
 PT CpG oligodeoxynucleotide.
 XX
 PS Example 7; SEQ ID NO 21; 37pp; English.
 XX

CC The present invention describes a method for inducing the production of
 CC vascular endothelial growth factor (VEGF) by a cell comprising contacting
 CC the cell with a CpG oligonucleotide and therefore inducing the production
 CC of VEGF by the cell. Also described: (1) inducing neovascularisation in a
 CC tissue, comprising introducing a CpG oligonucleotide into an area of the
 CC tissue where the formation of new blood vessels is desired, and so
 CC inducing neovascularisation in the area of the tissue; (2) promoting
 CC angiogenesis in an area of the subject where angiogenesis is desired,
 CC comprising introducing a CpG oligonucleotide to the area, and so
 CC promoting angiogenesis in the subject; and (3) screening for an agent
 CC that inhibits neovascularisation, comprising administering a CpG
 CC oligonucleotide to a non-human mammal and administering the agent to the
 CC mammal, where inhibition of angiogenesis in the animal indicates that the
 CC agent is effective in inhibiting neovascularisation. The CpG
 CC oligonucleotides have vulnerary, vasotropic and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The method and the CpG
 CC oligonucleotides can be used in inducing angiogenesis or
 CC neovascularisation, such as in subjects with a skin graft, subjects who
 CC exhibit male pattern baldness, or subjects who have a wound or who have
 CC atherosclerosis or ischaemia. The method may also be used in screening
 CC for agents that inhibit neovascularisation. The present sequence
 CC represents a CpG oligonucleotide which is used in the exemplification of
 CC the present invention.
 XX

SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
 |||||
 Db 3 TGCATCGACGCGGGGG 20

RESULT 9
 ABL35605
 ID ABL35605 standard; DNA; 28 BP.
 XX
 AC ABL35605;
 XX
 DT 04-APR-2002 (first entry)
 XX
 DE Immunostimulatory oligonucleotide SEQ ID NO: 531.
 XX
 KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
 KW infection; allergy; cancer; hypersensitivity; bio-warfare;
 KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
 KW immunosuppressive; protozoicide; virucide; hepatotropic; gene therapy;
 KW antiinflammatory; antibacterial; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_RNA 1..28
 FT /*tag= a
 FT /note= "optionally thymidine is replaced by uracil to
 FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
 FT least one other base through a ribose sugar"
 XX
 PN WO200193902-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 07-JUN-2001; 2001WO-US018276.
 XX
 PR 07-JUN-2000; 2000US-0209797P.
 XX
 PA (BIOS-) BIOSYNEXUS INC.
 XX
 PI Mond JJ, Flora M, Klinman DM;
 XX
 DR WPI; 2002-130570/17.
 XX

CC New immunostimulatory compositions comprising RNA/DNA hybrid
 CC oligonucleotides, useful for enhancing an immune response or inducing
 CC cytokines, particularly for treating diseases, e.g. cancer, allergy or
 CC HIV infection.
 XX

PS Example 11; Page 61; 68pp; English.

CC The present invention relates to an immunostimulatory composition, which
 CC comprises at least one oligonucleotide comprising both an RNA region and
 CC a DNA region. The composition is useful for enhancing an immune response
 CC or inducing cytokines. It can be used as a vaccine adjuvant and in
 CC treating diseases, including pathogenic infection, (non-)malignant
 CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
 CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
 CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
 CC hepatitis, HIV or malaria. The composition is also useful for treating,
 CC preventing or ameliorating the symptoms resulting from exposure to a bio-
 CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
 CC an immunostimulatory oligonucleotide described in the exemplification of
 CC the invention
 XX

SQ Sequence 28 BP; 5 A; 6 C; 12 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
 |||||

Db 11 TGCATCGACGCGGGGG 28

RESULT 10

ABL35593

ID ABL35593 standard; DNA; 28 BP.

XX AC ABL35593;

XX AC ABL35593;

XX DT 04-APR-2002 (first entry)

XX DE Immunostimulatory oligonucleotide SEQ ID NO: 519.

XX KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;

XX KW infection; allergy; cancer; hypersensitivity; bio-warfare;

XX KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;

XX KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;

XX KW antiinflammatory; antibacterial; ss.

XX OS Synthetic.

XX FH Key

XX FT Location/Qualifiers

XX FT 1. 28

XX FT misc_RNA

XX FT /*tag= a

XX FT /note= "optionally thymidine is replaced by uracil to

XX FT form RNA or DNA/RNA hybrids. Thymidine is linked to at

XX FT least one other base through a ribose sugar"

XX PN WO200193902-A2.

XX PD 13-DEC-2001.

XX PF 07-JUN-2001; 2001WO-US018276.

XX PR 07-JUN-2000; 2000US-0209797P.

XX PA (BIOS-) BIOSYNEXUS INC.

XX PI Mond JJ, Flora M, Klinman DM;

XX WPI; 2002-130570/17.

XX KW New immunostimulatory compositions comprising RNA/DNA hybrid

XX PT oligonucleotides, useful for enhancing an immune response or inducing

XX PT cytokines, particularly for treating diseases, e.g. cancer, allergy or

XX PT HIV infection.

XX Example 11; Page 61; 68pp; English.

XX The present invention relates to an immunostimulatory composition, which

XX comprises at least one oligonucleotide comprising both an RNA region and

XX a DNA region. The composition is useful for enhancing an immune response

XX or inducing cytokines. It can be used as a vaccine adjuvant and in

XX treating diseases, including pathogenic infection, (non-)malignant

XX tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or

XX colon, or carcinomas and sarcomas), autoimmune diseases or allergies

XX (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,

XX hepatitis, HIV or malaria. The composition is also useful for treating,

XX preventing or ameliorating the symptoms resulting from exposure to a bio-

XX warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is

XX an immunostimulatory oligonucleotide described in the exemplification of

XX the invention

XX Sequence 28 BP; 11 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 18; DB 6; Length 28;

XX Best Local Similarity 100.0%; Pred. No. 11;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18

Db 3 TGCATCGACGCGGGGG 20

RESULT 11

AAC80668

ID AAC80668 standard; DNA; 19 BP.

XX AC AAC80668;

XX DT 14-FEB-2001 (first entry)

XX DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:88.

XX KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;

XX KW immunogenic; cytokine release; natural killer cell; NK cell activation;

XX KW cell-mediated immune response; T-cell response; humoral response;

XX KW B-cell response; antibody production; immune response induction; vaccine;

XX KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;

XX KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;

XX KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;

XX KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;

XX KW antimicrobial; antiallergic; protozoacide; tuberculostatic;

XX KW antiasthmatic; dermatological; phosphorothioate; ss.

XX OS Synthetic.

XX PN WO2000061151-A2.

XX PD 19-OCT-2000.

XX PF 12-APR-2000; 2000WO-US009839.

XX PR 12-APR-1999; 99US-0128898P.

XX PA (KLIN/) KLINMAN D.

XX PA (ISHI/) ISHII K.

XX PA (VERT/) VERTHELYI D.

XX PI Klinman D, Ishii K, Verthelyi D;

XX WPI; 2001-006880/01.

XX Novel oligonucleotides useful for the prevention and treatment of

XX allergies, cancer, and autoimmune disorders and for ameliorating symptoms

XX resulting from exposure to a bio-warfare agent.

XX Claim 4; Page 37; 46pp; English.

XX The invention relates to novel immunogenic CpG oligodeoxynucleotides

XX (AAC80668-C80723). The oligonucleotides are at least 10 bases long and

XX comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY

XX -3'. The central CpG motif is unmethylated, and the oligonucleotides

XX optionally have phosphorothioate linkages which make them more resistant

XX to degradation. The invention also relates to an oligonucleotide delivery

XX complex comprising an oligonucleotide of the invention and a targeting

XX agent, and a pharmaceutical composition comprising the oligonucleotide

XX delivery complex. The oligonucleotides are able to induce either a cell-

XX mediated (T-cell) response or a humoral (B-cell, antibody) response, with

XX oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a

XX cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'

XX being able to induce a humoral response. It is thought that after

XX administration, the oligonucleotide acts on antigen-presenting cells

XX (e.g., macrophages and dendritic cells), which then release cytokines,

XX leading to activation of natural killer (NK) cells. A cell-mediated or

XX humoral response can then occur by activation of T- or B-cells. The

XX induction of an immune response is useful for treating, preventing or

XX ameliorating an allergic reaction (preferably asthma), or an infection,

XX where an immunogenic CpG oligonucleotide is administered either alone or

XX in combination with an anti-allergenic agent or anti-infectious agent.

XX The allergic conditions which may be treated include eczema, allergic

XX rhinitis, hayfever, urticaria, food allergies and other atopic

XX conditions, and the infections which may be treated include viral,

XX bacterial, fungal and protozoal infections such as tuberculosis, AIDS,

XX leishmania and schistosomiasis. Immune response induction may also be

XX used in the treatment of an autoimmune disorder (e.g., lupus

erythematous, rheumatoid arthritis and multiple sclerosis), a disease associated with immune system deficiency, and symptoms resulting from exposure to an agent of biological warfare. An immunogenic CpG oligonucleotide, either alone or in combination with an anti-cancer agent, is useful for treating solid tumour cancer. The induction of an immune response is used in antisense therapy and to improve the efficacy of a vaccine. The oligonucleotide is preferably administered to lymphocytes ex vivo, producing activated lymphocytes which are then administered to the host. The present sequence represents an immunogenic CpG oligodeoxynucleotide of the invention

Sequence 19 BP; 3 A; 4 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 94.4%; Score 17; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGGGG 17
Db 3 TGCATCGACGCGGGG 19

RESULT 12

AAS09638

ID AAS09638 standard; DNA; 19 BP.

AC AAS09638;

XX 26-SEP-2001 (first entry)

XX Immunoreactive CpG sequence-containing oligonucleotide #88.

XX CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.

XX Synthetic.

XX WO200151500-A1.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-US001122.

XX 14-JAN-2000; 2000US-0176115P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Klinman D, Ishii K, Verthelyi D;

XX WPI; 2001-442129/47.

XX Oligodeoxynucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG sequences.

XX Claim 5; Page 41; 48pp; English.

XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10 nucleotides comprising multiple CpG sequences, where one of the CpG sequences is different from another of the multiple CpG sequences. The ODN are useful for inducing an immune response, preferably a cell-mediated immune response, involving non-B cell activation, interferon gamma (IFN-gamma) production or a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host for treating, preventing or ameliorating an allergic reaction, e.g. asthma,

CC cancer, e.g. solid tumour cancer, a disease associated with the immune system e.g. autoimmune disorder or an immune system deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antisense therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions for improving the efficacy of vaccines against hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, Anthrax and Listeria

Sequence 19 BP; 3 A; 4 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 94.4%; Score 17; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGGGG 17
Db 3 TGCATCGACGCGGGG 19

RESULT 13

ABK46516

ID ABK46516 standard; DNA; 19 BP.

XX ABK46516;

XX 05-JUN-2002 (first entry)

XX Immunostimulatory unmethylated CpG oligodeoxynucleotide #106.

XX unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine;

XX Paramyxoviridae; F protein; respiratory syncytial virus; RSV;

XX viral bronchiolitis; pneumonia; infectious pulmonary disease;

XX bronchopulmonary dysplasia; congenital heart condition; ss.

XX Synthetic.

XX WO200211761-A2.

XX 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US041633.

XX 10-AUG-2000; 2000US-0224011P.

XX 01-SEP-2000; 2000US-0229307P.

XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

XX Mond JJ, Prince G, Klinman DM;

XX WPI; 2002-227118/28.

XX Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of Paramyxoviridae F protein, and cytosine followed by guanine linked by phosphate bond-oligodeoxynucleotides.

XX Claim 4; Page 9; 30pp; English.

XX The invention describes a vaccine comprising one or more epitopes of a Paramyxoviridae F protein, and one or more CpG (cytosine followed by guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The vaccine is useful for vaccinating a patient especially against viruses of the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the primary cause of viral bronchiolitis and pneumonia in infants and children, and infectious pulmonary disease in infants. RSV has been particularly implicated in death of infants that are premature, have

CC bronchopulmonary dysplasia, or congenital heart conditions. This sequence
CC represents an oligonucleotide that can be used in the creation of
CC the vaccine

XX
SQ Sequence 19 BP; 3 A; 4 C; 10 G; 2 T; 0 U; 0 Other;
Query Match 94.4%; Score 17; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATGACGACGAGGGG 17
|||||
Db 3 TGCATGACGACGAGGGG 19

RESULT 14
ABL35587
ID ABL35587 standard; DNA; 18 BP.

XX AC ABL35587;
XX DT 04-APR-2002 (first entry)
XX DE Immunostimulatory oligonucleotide SEQ ID NO: 513.
XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX infection; allergy; cancer; hypersensitivity; bio-warfare;
XX immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX antiinflammatory; antibacterial; ss.
XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT misc_RNA 1..18
XX FT /*tag= a
XX FT /note= "optionally thymidine is replaced by uracil to
XX FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
XX FT least one other base through a ribose sugar"

XX PN WO200193902-A2.

XX PD 13-DEC-2001.

XX PF 07-JUN-2001; 2001WO-US018276.

XX PR 07-JUN-2000; 2000US-0209797P.

XX PA (BIOS-) BIOSYNEXUS INC.

XX PI Mond JJ, Flora M, Kliman DM;

XX DR WPI; 2002-130570/17.

XX New immunostimulatory compositions comprising RNA/DNA hybrid
XX oligonucleotides, useful for enhancing an immune response or inducing
XX cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX HIV infection.

XX Example 11; Page 61; 68pp; English.

XX The present invention relates to an immunostimulatory composition, which
XX comprises at least one oligonucleotide comprising both an RNA region and
XX a DNA region. The composition is useful for enhancing an immune response
XX or inducing cytokines. It can be used as a vaccine adjuvant and in
XX treating diseases, including pathogenic infection, (non-)malignant
XX tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX hepatitis, HIV or malaria. The composition is also useful for treating,
XX preventing or ameliorating the symptoms resulting from exposure to a bio-
XX warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX an immunostimulatory oligonucleotide described in the exemplification of

CC the invention

XX SQ Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 6; Length 18;
Best Local Similarity 94.4%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATGACGACGAGGGG 18
|||||
Db 1 TGCATGACGACGAGGGG 18

RESULT 15

ABL35577
ID ABL35577 standard; DNA; 18 BP.

XX AC ABL35577;

XX DT 04-APR-2002 (first entry)

XX DE Immunostimulatory oligonucleotide SEQ ID NO: 503.

XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX infection; allergy; cancer; hypersensitivity; bio-warfare;
XX immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX antiinflammatory; antibacterial; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT misc_RNA 1..18
XX FT /*tag= a
XX FT /note= "optionally thymidine is replaced by uracil to
XX FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
XX FT least one other base through a ribose sugar"

XX PN WO200193902-A2.

XX PD 13-DEC-2001.

XX PF 07-JUN-2001; 2001WO-US018276.

XX PR 07-JUN-2000; 2000US-0209797P.

XX PA (BIOS-) BIOSYNEXUS INC.

XX PI Mond JJ, Flora M, Kliman DM;

XX DR WPI; 2002-130570/17.

XX New immunostimulatory compositions comprising RNA/DNA hybrid
XX oligonucleotides, useful for enhancing an immune response or inducing
XX cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX HIV infection.

XX Example 11; Page 61; 68pp; English.

XX The present invention relates to an immunostimulatory composition, which
XX comprises at least one oligonucleotide comprising both an RNA region and
XX a DNA region. The composition is useful for enhancing an immune response
XX or inducing cytokines. It can be used as a vaccine adjuvant and in
XX treating diseases, including pathogenic infection, (non-)malignant
XX tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX hepatitis, HIV or malaria. The composition is also useful for treating,
XX preventing or ameliorating the symptoms resulting from exposure to a bio-
XX warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX an immunostimulatory oligonucleotide described in the exemplification of
XX the invention

SQ Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 91.1%; Score 16.4; DB 6; Length 18;
Best Local Similarity 94.4%; Pred. NO. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGCATCGACGCGAGGGGG 18
| | | | | | | | | | | | | | | | | |
Db 1 TGCATCGATCGACGAGGGGG 18

Search completed: July 2, 2004, 08:31:38
Job time : 134.89 secs

QY 1 TGCATCGACGAGGGGG 18
 Db 97 TGCATCGACGAGGGGG 114

RESULT 3
 AV269637
 LOCUS
 DEFINITION
 AV269637
 AV269637
 AV269637.1 GI:6257674
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 303)
 Konno.H., Aizawa.K., Akahira.S., Akiyama.J., Carninci.P., Endo.T.,
 Fukuda.S., Fukunishi.Y., Hara.A., Hayatsu.N., Hirozane.F., Hori.F.,
 Ishii.Y., Ishikawa.T., Itoh.M., Izawa.M., Kadota.K., Kagawa.I.,
 Kai.C., Kawai.J., Kikuchi.N., Kojima.Y., Koya.S., Kusakabe.M.,
 Matsuyama.T., Miki.R., Mizuno.Y., Nakamura.M., Oda.H., Okazaki.Y.,
 Owa.C., Ozawa.Y., Saito.H., Sano.M., Sato.K., Shibata.K.,
 Shibata.Y., Shigemoto.Y., Shiraki.T., Sogabe.Y., Sugahara.Y.,
 Suzuki.H., Suzuki.H., Takahashi.F., Tateno.M., Tomimaga.N.,
 Tsunoda.Y., Wakahiki.A., Watanabe.S., Yamamura.T., Yasunishi.A.,
 Yokota.T., Yoshiki.A., Yoshino.M., Muramatsu.M. and Hayashizaki.Y.
 RIKEN Mouse ESTs (Konno.H., et al. 1999)
 Unpublished (1999)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@res.riken.go.jp/
 URL: http://genome.gsc.riken.go.jp/
 Sasaki.N., Izawa.M., Watahiki.X., Ozawa.K., Tanaka.T., Yoneda.Y.,
 Matsura.S., Carninci.P., Muramatsu.M., Okazaki.Y. and
 Hayashizaki.Y.
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
 Itoh.M., Kitsumi.T., Akiyama.J., Shibata.K., Izawa.M., Kawai.J.,
 Tomaru.Y., Carninci.P., Shibata.Y., Ozawa.Y., Muramatsu.M.,
 Okazaki.Y. and Hayashizaki.Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci.P. and Hayashizaki.Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

FEATURES
 source
 1. .303
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="493054G09"
 /sex="male"
 /tissue_type="testis"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, adult male testis
 (DH10B)"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was

ORIGIN
 Query Match 91.1%; Score 16.4; DB 9; Length 303;
 Best Local Similarity 94.4%; Pred. No. 4.2e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCATCGACGAGGGGG 18
 Db 143 TGCATCGACGAGGGGG 160

RESULT 4
 AV269637
 LOCUS
 DEFINITION
 AV269637
 AV269637.1 GI:5797774
 EST.
 Mus musculus (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 410)
 Mahairas.G.G., Wallace.J.C., Smith.K., Swartzell.S., Holzman.T.,
 Keller.A., Shaker.R., Furlong.J., Young.J., Zhao.S., Adams.M.D. and
 Hood.L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 99380589
 10449764
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 2087 row: E column: 13
 Seq primer: 77
 Class: BAC ends
 High quality sequence stop: 410.
 Location/Qualifiers
 1. 410
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=2087 Col=13 Row=E"
 /sex="male"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBelOAG11; BAC Clones in
 E-Coli DH10B"

ORIGIN
 Query Match 91.1%; Score 16.4; DB 28; Length 410;
 Best Local Similarity 94.4%; Pred. No. 4.5e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCATCGACGAGGGGG 19

QY 1 TGCATCGACGAGGGGG 18
 Db 97 TGCATCGACGAGGGGG 114

RESULT 3
 AV269637
 LOCUS
 DEFINITION
 AV269637
 AV269637
 AV269637.1 GI:6257674
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 303)
 Konno.H., Aizawa.K., Akahira.S., Akiyama.J., Carninci.P., Endo.T.,
 Fukuda.S., Fukunishi.Y., Hara.A., Hayatsu.N., Hirozane.F., Hori.F.,
 Ishii.Y., Ishikawa.T., Itoh.M., Izawa.M., Kadota.K., Kagawa.I.,
 Kai.C., Kawai.J., Kikuchi.N., Kojima.Y., Koya.S., Kusakabe.M.,
 Matsuyama.T., Miki.R., Mizuno.Y., Nakamura.M., Oda.H., Okazaki.Y.,
 Owa.C., Ozawa.Y., Saito.H., Sano.M., Sato.K., Shibata.K.,
 Shibata.Y., Shigemoto.Y., Shiraki.T., Sogabe.Y., Sugahara.Y.,
 Suzuki.H., Suzuki.H., Takahashi.F., Tateno.M., Tomimaga.N.,
 Tsunoda.Y., Wakahiki.A., Watanabe.S., Yamamura.T., Yasunishi.A.,
 Yokota.T., Yoshiki.A., Yoshino.M., Muramatsu.M. and Hayashizaki.Y.
 RIKEN Mouse ESTs (Konno.H., et al. 1999)
 Unpublished (1999)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@res.riken.go.jp/
 URL: http://genome.gsc.riken.go.jp/
 Sasaki.N., Izawa.M., Watahiki.X., Ozawa.K., Tanaka.T., Yoneda.Y.,
 Matsura.S., Carninci.P., Muramatsu.M., Okazaki.Y. and
 Hayashizaki.Y.
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
 Itoh.M., Kitsumi.T., Akiyama.J., Shibata.K., Izawa.M., Kawai.J.,
 Tomaru.Y., Carninci.P., Shibata.Y., Ozawa.Y., Muramatsu.M.,
 Okazaki.Y. and Hayashizaki.Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci.P. and Hayashizaki.Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

FEATURES
 source
 1. .303
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="493054G09"
 /sex="male"
 /tissue_type="testis"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, adult male testis
 (DH10B)"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was

ORIGIN
 Query Match 91.1%; Score 16.4; DB 9; Length 303;
 Best Local Similarity 94.4%; Pred. No. 4.2e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCATCGACGAGGGGG 18
 Db 143 TGCATCGACGAGGGGG 160

RESULT 4
 AV269637
 LOCUS
 DEFINITION
 AV269637
 AV269637.1 GI:5797774
 EST.
 Mus musculus (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 410)
 Mahairas.G.G., Wallace.J.C., Smith.K., Swartzell.S., Holzman.T.,
 Keller.A., Shaker.R., Furlong.J., Young.J., Zhao.S., Adams.M.D. and
 Hood.L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 99380589
 10449764
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 2087 row: E column: 13
 Seq primer: 77
 Class: BAC ends
 High quality sequence stop: 410.
 Location/Qualifiers
 1. 410
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=2087 Col=13 Row=E"
 /sex="male"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBelOAG11; BAC Clones in
 E-Coli DH10B"

ORIGIN
 Query Match 91.1%; Score 16.4; DB 28; Length 410;
 Best Local Similarity 94.4%; Pred. No. 4.5e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCATCGACGAGGGGG 19

[illegible]

/clone lib="ZM 0.6 1.0 KB"
/note="Vector: PCR4-toFO; Site 1: EcoRI; 0.6-1.0 kb high
Cor selected genomic DNA library"

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 888;
Best Local Similarity 94.4%; Pred. No. 5.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 314 TCCATCGACGCGGGGG 297

RESULT 8
CG225423/C

LOCUS CG225423 960 bp DNA linear GSS 22-AUG-2003
DEFINITION CG2AN65TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0744K10,
genomic survey sequence.

ACCESSION

VERSION CG225423
KEYWORDS GSS.

SOURCE

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 960)

REFERENCE

AUTHORS

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)

TITLE

JOURNAL

COMMENT

Other GSSs: CG2AN65TH

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TP

Class: sheared ends.

Location/Qualifiers

1..960

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone lib="ZM 0.7 1.5 KB"

/note="Vector: pBCSK; Site 1: HincII; 0.7-1.5 kb

methylation filtered genomic DNA library"

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 960;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
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Db 947 TCCATCGACGCGGGGG 930

RESULT 9

CC655225

LOCUS

CC655225 980 bp DNA linear GSS 19-JUN-2003

DEFINITION CGUL070TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0469K19,
genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 980)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)

Other GSSs: CGUL070TH

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TP

Class: sheared ends.

Location/Qualifiers

1..980

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone lib="ZM 0.7 1.5 KB"

/note="Vector: pBCSK; Site 1: HincII; 0.7-1.5 kb

methylation filtered genomic DNA library"

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 980)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)

Other GSSs: CGUL070TH

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TP

Class: sheared ends.

Location/Qualifiers

1..980

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone lib="ZM 0.7 1.5 KB"

/note="Vector: pBCSK; Site 1: HincII; 0.7-1.5 kb

methylation filtered genomic DNA library"

FEATURES

source

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

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Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

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Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 295

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</

/mol_type="mRNA"
 /db_xref="GDB:1247962"
 /db_xref="taxon:9606"
 /clone="IMAGE:303030"
 /dev_stage="19 weeks"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares fetal_lung_NbH19M"
 /note="Organ: lung; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCACTCGAAGTGGGCGCGCAATTTTCTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbH19M."

ORIGIN

Query Match 85.6%; Score 15.4; DB 14; Length 435;
 Best Local Similarity 94.1%; Pred. No. 1.3e+04;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCATCGACGCGGGGG 18
 | ||||| ||||| |||||
 Db 388 GGATCGACGCGGGGG 404

RESULT 13

CG714924 468 bp DNA linear GSS 20-OCT-2003
 LOCUS 1119039804.y1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.

ACCESSION CG714924
 VERSION GSS.
 KEYWORDS
 SOURCE

ORGANISM

Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 468)

Walbot, V.
 Maize genomic sequences found using engineered RescueMu transposon

REFERENCE

Unpublished (2001)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221

Email: walbot@stanford.edu
 Possible ligation site so sequence was trimmed. Post-ligation sequence submitted separately.
 Plate: 1119039 row: 42
 Class: transposon-tagged.

FEATURES

source

1..468
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/X55"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="1119 - RescueMu Grid AA"

/note="Organ: leaf; Vector: RescueMu (engineered from Bluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 Kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 85.6%; Score 15.4; DB 29; Length 468;
 Best Local Similarity 94.1%; Pred. No. 1.3e+04;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCATCGACGCGGGGG 18
 | ||||| ||||| |||||
 Db 17 GCATCGACGCGGGGG 33

RESULT 14

BI507147/c

LOCUS

DEFINITION BI507147 473 bp mRNA linear EST 08-APR-2002
 BI170025B20H07.5 Bee Brain Normalized/Subtracted Library, BB17 Apis mellifera cDNA clone BB170025B20H07 5', mRNA sequence.

ACCESSION

BI507147

VERSION

BI507147.1 GI:15357521

KEYWORDS

Apis mellifera (honeybee)

SOURCE

Apis mellifera

ORGANISM

Apis mellifera

REFERENCE

1 (bases 1 to 473)

AUTHORS

Whitfield, C.W., Bonaldo, M.F., Kumar, C.G., Liu, L.,

Pardinas, J., Robertson, H.M., Soares, B. and Robinson, G.E.

Annotated expressed sequence tags and cDNA microarrays for studies of brain and behavior in the honey bee

Genome Res. 12 (4), 555-566 (2002)

21929762

11932240

Contact: Gene E. Robinson

Department of Entomology

University of Illinois

505 S. Goodwin Ave., Urbana, IL 61801, USA

Tel: 217 265 0309

Fax: 217 244 3499

Email: generobi@life.uiuc.edu

This research was funded by the University of Illinois Critical

Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation

Award in Functional Genomics to G.E. Robinson and an NSF

Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.

REPEAT IN THE SEQUENCE

Simple repeat STRAND (+) ELEMENT (A)n LOCATION [449,468].

PCR Primers

FORWARD: TAATACGACTCACTATAGG

BACKWARD: ATTACCTCACTAAG

Plate: BB170025B20 row: H column: 07

Seq primer: AGCGATAACAAATTCACACAGGA

High quality sequence stop: 473.

Location/Qualifiers

1..473

/organism="Apis mellifera"

/mol_type="mRNA"

/strain="mixed strains of European bees, predominantly

A.m. ligustica"

/db_xref="taxon:7460"

/clone="BB170025B20H07"

/sex="female"

/tissue_type="brain"

/dev_stage="adult worker honey bee"

/lab_host="DH10B"

/clone_lib="Bee Brain Normalized/Subtracted Library, BB17"

/note="Organ: Brain; Vector: pT73-Pac; Site 1: EcoRI;

Site 2: NotI; This BB17 cDNA library was generated by

subtraction of the BB16 library with 4000 previously sequenced clones. The BB16 library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups."

ORIGIN

Query Match 85.6%; Score 15.4; DB 12; Length 473;
Best Local Similarity 94.1%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCATCGACGACGAGGGG 17
Db 334 TGCATCGACGACGAGGGG 318

RESULT 15

AI812904 504 bp mRNA linear EST 08-JUL-1999
LOCUS 22C9 Pine Lambda Zap Xylem library Pinus taeda CDNA, mRNA sequence.
DEFINITION
ACCESSION AI812904
VERSION AI812904.1 GI:5424255
KEYWORDS EST.
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 504)
REFERENCE Whetten, R.W., Kinlaw, C.S., Retzel, B. and Sederoff, R.R.
TITLE The Pine Gene Discovery Project
JOURNAL Unpublished (1999)
COMMENT Contact: Ross Whetten
Forest Biotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall,
Raleigh, NC, 27695-8008
Tel: 919-515-7800
Fax: 919-515-7801
Email: rosswhet@unity.ncsu.edu
Seq primer: T3.

FEATURES

source 1..504
Location/Qualifiers
/organism="Pinus taeda"
/mol_type="mRNA"
/db_xref="taxon:3352"
/tissue_type="differentiating xylem"
/clone_lib="Pine Lambda Zap Xylem library"
/note="Vector: Lambda Zap; Site 1: EcoRI; Site 2: XhoI;
Differentiating xylem was collected from the main stem of a 35-year old loblolly pine tree harvested during the growing season. RNA isolation and library preparation followed the methods of Allona et al., PNAS 95:9693-8, 1998"

ORIGIN

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Best Local Similarity 94.1%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCATCGACGACGAGGGG 17
Db 170 TGCATCGACGACGAGGGG 186

Search completed: July 2, 2004, 13:33:11
Job time : 1351.14 secs

OM nucleic - nucleic search, using sw model
Run on: July 2, 2004, 07:36:05 ; Search time 633.732 Seconds
(without alignments)
1231.080 Million cell updates/sec

Title: US-10-068-160-19
Perfect score: 18
Sequence: 1 tgcacgcagcagggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: gb_ba.*
2: gb_hg.*
3: gb_in.*
4: gb_m.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pt.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
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27: em_sts.*
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30: em_htg_hum.*
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32: em_htg_other.*
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37: em_htg_vrt.*
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41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	100.0	20	6	AX194500	AX194500 Sequence
2	18	100.0	20	6	AX352202	AX352202 Sequence
3	18	100.0	20	6	AX352213	AX352213 Sequence
4	18	100.0	20	6	AX352246	AX352246 Sequence
5	18	100.0	28	6	AX352223	AX352223 Sequence
6	18	100.0	28	6	AX352235	AX352235 Sequence
7	17	94.4	19	6	AX194488	AX194488 Sequence
8	17	94.4	19	6	AX465438	AX465438 Sequence
9	16.4	91.1	18	6	AX352207	AX352207 Sequence
10	16.4	91.1	18	6	AX352217	AX352217 Sequence
11	16.4	91.1	18	6	AX352255	AX352255 Sequence
12	16.4	91.1	20	6	AX194432	AX194432 Sequence
13	16.4	91.1	20	6	AX194434	AX194434 Sequence
14	16.4	91.1	20	6	AX194437	AX194437 Sequence
15	16.4	91.1	20	6	AX194438	AX194438 Sequence
16	16.4	91.1	20	6	AX194439	AX194439 Sequence
17	16.4	91.1	20	6	AX194441	AX194441 Sequence
18	16.4	91.1	20	6	AX194443	AX194443 Sequence
19	16.4	91.1	20	6	AX194472	AX194472 Sequence
20	16.4	91.1	20	6	AX352198	AX352198 Sequence
21	16.4	91.1	20	6	AX352206	AX352206 Sequence
22	16.4	91.1	20	6	AX352209	AX352209 Sequence
23	16.4	91.1	20	6	AX352216	AX352216 Sequence
24	16.4	91.1	20	6	AX352242	AX352242 Sequence
25	16.4	91.1	20	6	AX352250	AX352250 Sequence
26	16.4	91.1	20	6	AX352254	AX352254 Sequence
27	16.4	91.1	20	6	AX465382	AX465382 Sequence
28	16.4	91.1	20	6	AX465384	AX465384 Sequence
29	16.4	91.1	20	6	AX465387	AX465387 Sequence
30	16.4	91.1	20	6	AX465388	AX465388 Sequence
31	16.4	91.1	20	6	AX465389	AX465389 Sequence
32	16.4	91.1	20	6	AX465391	AX465391 Sequence
33	16.4	91.1	20	6	AX465393	AX465393 Sequence
34	16.4	91.1	20	6	AX465422	AX465422 Sequence
35	16.4	91.1	20	6	AX816067	AX816067 Sequence
36	16.4	91.1	22	6	AX352204	AX352204 Sequence
37	16.4	91.1	22	6	AX352248	AX352248 Sequence
38	16.4	91.1	26	6	AX352228	AX352228 Sequence
39	16.4	91.1	26	6	AX352240	AX352240 Sequence
40	16.4	91.1	28	6	AX352219	AX352219 Sequence
41	16.4	91.1	28	6	AX352227	AX352227 Sequence
42	16.4	91.1	28	6	AX352231	AX352231 Sequence
43	16.4	91.1	28	6	AX352239	AX352239 Sequence
44	16.4	91.1	29	6	AX352237	AX352237 Sequence
45	16.4	91.1	30	6	AX352225	AX352225 Sequence

ALIGNMENTS

RESULT 1
AX194500
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AX194500
Sequence 100 from Patent WO0151500.
AX194500
AX194500.1 GI:15385156

synthetic construct
synthetic construct
artificial sequences.

1
Kliman,D., Ishii,K. and Verthelyi,D.
Oligodeoxynucleotide and its use to induce an immune response
Patent: WO 0151500-A 100 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)

Pred. No. is the number of results predicted by chance to have a

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  3 TGCATCGACGACGAGGGGG 20

Db

RESULT 2
AX352202
LOCUS
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    Sequence 498 from Patent WO0193902.
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  VERSION
    AX352202.1 GI:18617495
  KEYWORDS
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  SOURCE
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    synthetic construct
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  ORGANISM
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  REFERENCE
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      AUTHORS
        Mond, J.J., Flora, M. and Klinman, D.M.
      TITLE
        Immunostimulatory rna/dna hybrid molecules
      JOURNAL
        Patent: WO 0193902-A 498 13-DEC-2001;
        Biosynexus Incorporated (US)
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QY
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    |||||
  3 TGCATCGACGACGAGGGGG 20

Db

RESULT 3
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LOCUS
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  ACCESSION
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  VERSION
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  KEYWORDS
    .
  SOURCE
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    synthetic construct
    artificial sequences.
  ORGANISM
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  REFERENCE
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      AUTHORS
        Mond, J.J., Flora, M. and Klinman, D.M.
      TITLE
        Immunostimulatory rna/dna hybrid molecules
      JOURNAL
        Patent: WO 0193902-A 509 13-DEC-2001;
        Biosynexus Incorporated (US)
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ORIGIN
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QY
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  3 TGCATCGACGACGAGGGGG 20

Db

RESULT 4
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LOCUS
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    AX352246.1 GI:18617529
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      AUTHORS
        Mond, J.J., Flora, M. and Klinman, D.M.
      TITLE
        Immunostimulatory rna/dna hybrid molecules
      JOURNAL
        Patent: WO 0193902-A 542 13-DEC-2001;
        Biosynexus Incorporated (US)
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  3 TGCATCGACGACGAGGGGG 20

Db

RESULT 5
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    AX352223
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    AX352223.1 GI:18617506
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    artificial sequences.
  ORGANISM
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      AUTHORS
        Mond, J.J., Flora, M. and Klinman, D.M.
      TITLE
        Immunostimulatory rna/dna hybrid molecules
      JOURNAL
        Patent: WO 0193902-A 519 13-DEC-2001;
        Biosynexus Incorporated (US)
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  3 TGCATCGACGACGAGGGGG 20

Db

RESULT 6

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AX352235
LOCUS AX352235 28 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence S31 from Patent WO0193902.
ACCESSION AX352235
VERSION AX352235.1 GI:18617518
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
  1 Mond, J.J., Flora, M. and Klinman, D.M.
  TITLE Immunostimulatory rna/dna hybrid molecules
  JOURNAL Patent: WO 0193902-A 531 13-DEC-2001;
  Biosynexus Incorporated (US)
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 11 TGCATCGACGCGGGGG 28
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RESULT 7
AX194488
LOCUS AX194488 19 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 88 from Patent WO0151500.
ACCESSION AX194488
VERSION AX194488.1 GI:15385144
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
  1 Klinman, D., Ishii, K. and Verthelyi, D.
  TITLE Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL Patent: WO 0151500-A 88 19-JUL-2001;
  Secretary of the Department of Health and Human Services (US)
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGGGGG 17
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Db 3 TGCATCGACGCGGGGG 19
    |||||

RESULT 8
AX465438
LOCUS AX465438 19 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 106 from Patent WO0211761.
ACCESSION AX465438
VERSION AX465438.1 GI:21899801
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
  1 Mond, J.J., Flora, M. and Klinman, D.M.
  TITLE Immunostimulatory rna/dna hybrid molecules
  JOURNAL Patent: WO 0193902-A 513 13-DEC-2001;
  Biosynexus Incorporated (US)
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Best Local Similarity 94.4%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGGGGG 18
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Db 1 TGCATCGATCGCGGGGG 18
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RESULT 10
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LOCUS AX352217 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 513 from Patent WO0193902.
ACCESSION AX352217
VERSION AX352217.1 GI:18617500
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
  1 Mond, J.J., Flora, M. and Klinman, D.M.
  TITLE Immunostimulatory rna/dna hybrid molecules
  JOURNAL Patent: WO 0193902-A 513 13-DEC-2001;
  Biosynexus Incorporated (US)
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGGGGG 18
    |||||
Db 11 TGCATCGACGCGGGGG 28
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REFERENCE
  1 Mond, J.J., Prince, G. and Klinman, D.M.
  TITLE Vaccine against RSV
  JOURNAL Patent: WO 0211761-A 106 14-FEB-2002;
  HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
  MEDICINE (US)
FEATURES
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGGGGG 17
    |||||
Db 3 TGCATCGACGCGGGGG 19
    |||||

RESULT 9
AX352207
LOCUS AX352207 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 503 from Patent WO0193902.
ACCESSION AX352207
VERSION AX352207.1 GI:18617490
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
  1 Mond, J.J., Flora, M. and Klinman, D.M.
  TITLE Immunostimulatory rna/dna hybrid molecules
  JOURNAL Patent: WO 0193902-A 503 13-DEC-2001;
  Biosynexus Incorporated (US)
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ORIGIN
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Best Local Similarity 94.4%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGGGGG 18
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Db 1 TGCATCGATCGCGGGGG 18
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RESULT 11
AX352217
LOCUS AX352217 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 513 from Patent WO0193902.
ACCESSION AX352217
VERSION AX352217.1 GI:18617500
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
  1 Mond, J.J., Flora, M. and Klinman, D.M.
  TITLE Immunostimulatory rna/dna hybrid molecules
  JOURNAL Patent: WO 0193902-A 513 13-DEC-2001;
  Biosynexus Incorporated (US)
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    /note="Synthetic HDR"
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Best Local Similarity 94.4%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGGGGG 18
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ORIGIN

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Matches 17; Conservative 0; Mismatches 0;

QY 1 TGCATCGACGCGGGGG 18
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RESULT 11

AX194432
LOCUS AX352255 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 551 from Patent WO0193902.
ACCESSION AX352255
VERSION AX352255.1 GI:18617538
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mord, J.J., Floza, M. and Klimman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 551 13-DEC-2001;
Biosynexus Incorporated (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 18;
Best Local Similarity 94.4%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

QY 1 TGCATCGACGCGGGGG 18
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Db 1 TGCATCGATCGAGGGGG 18

RESULT 12

AX194432
LOCUS AX352255 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 32 from Patent WO0151500.
ACCESSION AX194432
VERSION AX194432.1 GI:15385088
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Klimman, D., Ishii, K. and Verthelyi, D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 32 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
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Best Local Similarity 94.4%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
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Db 3 TGCATCGATCGAGGGGG 20

RESULT 13

AX194434
LOCUS AX194434 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 34 from Patent WO0151500.
ACCESSION AX194434
VERSION AX194434.1 GI:15385090
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Klimman, D., Ishii, K. and Verthelyi, D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 34 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
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Db 3 TGCATCGATCGAGGGGG 20

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AX194437
LOCUS AX194437 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 37 from Patent WO0151500.
ACCESSION AX194437
VERSION AX194437.1 GI:15385093
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Klimman, D., Ishii, K. and Verthelyi, D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 37 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
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QY 1 TGCATCGACGCGGGGG 18
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Db 3 TGCATCGATCGAGGGGG 20

RESULT 15

AX194438
LOCUS AX194438 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 38 from Patent WO0151500.

ACCESSION AX194438
VERSION AX194438.1 GI:15385094
KEYWORDS
SOURCE Synthetic construct
ORGANISM Synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 38 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
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Db 3 TGCATCGATCGACGCGGG 20
Search completed: July 2, 2004, 10:08:10
Job time : 633.732 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:38:45 / Search time 1348.02 seconds
(without alignments)
398.746 Million cell updates/sec

US-10-068-160-19

Title:

Perfect score: 18

Sequence: 1 tgcacgcagcagggggg 18

Scoring table: IDENTITY_NUC

Gapop_10_0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

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8: em_htc.*

9: gb_est1.*

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11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_nam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

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27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	91.1	240	9	AV281636
2	16.4	91.1	257	9	AV268287
3	16.4	91.1	303	9	AV269637
4	16.4	91.1	410	28	AQ831712

5	16.4	91.1	693	12	EG853689
6	16.4	91.1	878	29	CG225411
c 7	16.4	91.1	888	29	CG458305
c 8	16.4	91.1	960	29	CG225423
9	16.4	91.1	980	29	CG655225
10	15.4	85.6	246	9	AV253772
11	15.4	85.6	355	13	BX566321
12	15.4	85.6	435	14	N91570
13	15.4	85.6	468	23	CG714924
c 14	15.4	85.6	473	12	BI507147
15	15.4	85.6	504	9	AI812904
16	15.4	85.6	523	28	AZ573909
17	15.4	85.6	524	28	AZ569840
18	15.4	85.6	554	14	CD216827
19	15.4	85.6	570	28	AZ568729
c 20	15.4	85.6	572	13	BX783110
21	15.4	85.6	572	13	BZ931640
22	15.4	85.6	574	14	CB186390
c 23	15.4	85.6	622	29	CE347538
24	15.4	85.6	709	14	CB031270
25	15.4	85.6	713	14	CB025221
c 26	15.4	85.6	807	13	CA101677
27	15.4	85.6	944	29	CNS02PE3
28	15.4	85.6	957	29	CG460886
29	15.4	85.6	971	29	CNS02WQO
c 30	15.4	85.6	1003	13	BQ708058
c 31	15.4	85.6	1011	29	CG460924
32	15.4	85.6	1207	12	BG722803
33	15.4	85.6	1522	10	AW729951
34	15	83.3	452	29	CG726899
35	15	83.3	480	29	CG721957
c 36	15	83.3	530	14	CB368184
c 37	15	83.3	572	12	BM175141
c 38	15	83.3	614	14	CD886393
39	15	83.3	687	14	CB026323
c 40	15	83.3	1147	9	AV715321
41	14.8	82.2	202	9	AV268789
42	14.8	82.2	228	10	BB016918
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44	14.8	82.2	245	9	AV256921
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ALIGNMENTS

RESULT 1

AV281636

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AV281636 AV281636 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus CDNA clone 4933425JUS 3', mRNA sequence.

musculus (house mouse)

EST.

GI:6269673

EST.

1 (bases 1 to 240)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, T., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tomimatsu, N., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Konno, H., et al. 1999)

Unpublished (1999)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

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  ACCESSION AX465426
  VERSION AX465426.1 GI:21899789
  KEYWORDS
  SOURCE
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    synthetic construct
    artificial sequences.
  REFERENCE
  1
  AUTHORS Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE Vaccine against RSV
  JOURNAL HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
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  KEYWORDS
  SOURCE
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    synthetic construct
    artificial sequences.
  REFERENCE
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  AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL Patent: WO 0151500-A 40 19-JUL-2001;
  Secretary of the Department of Health and Human Services (US)
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  ACCESSION AX194481
  VERSION AX194481.1 GI:15385137
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  REFERENCE
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  AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL Patent: WO 0151500-A 81 19-JUL-2001;
  Secretary of the Department of Health and Human Services (US)
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  ACCESSION AX194482
  VERSION AX194482.1 GI:15385138
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  AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL Patent: WO 0151500-A 82 19-JUL-2001;
  Secretary of the Department of Health and Human Services (US)
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artificial sequences.					
REFERENCE	1				
AUTHORS	Mond,J.J., Flora,M. and Klimman,D.M.				
TITLE	Immunostimulatory rna/dna hybrid molecules				
JOURNAL	Patent: WO 0193902-A 510 13-DEC-2001;				
FEATURES	Biosynexus Incorporated (US)				
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RESULT 9					
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LOCUS	AX352247	20 bp	DNA	linear	PAT 06-FEB-2002
DEFINITION	Sequence 543 from Patent WO0193902.				
ACCESSION	AX352247				
VERSION	AX352247.1 GI:18617530				
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1				
AUTHORS	Mond,J.J., Flora,M. and Klimman,D.M.				
TITLE	Immunostimulatory rna/dna hybrid molecules				
JOURNAL	Patent: WO 0193902-A 543 13-DEC-2001;				
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LOCUS	AX465390				
DEFINITION	Sequence 58 from Patent WO0211761.				
ACCESSION	AX465390				
VERSION	AX465390.1 GI:21899753				
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
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REFERENCE	1				
AUTHORS	Mond,J.J., Prince,G. and Klinman,D.M.				
TITLE	Vaccine against RSV				
JOURNAL	Patent: WO 0211761-A 58 14-FEB-2002;				
FEATURES	HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY MEDICINE (US)				
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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCCCGATGCAGGGGG 18
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Db 3 TCGTCGATGCAGGGGG 20

RESULT 11
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LOCUS AX465431 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 99 from Patent WO0211761.
ACCESSION AX465431
VERSION AX465431.1 GI:21899794
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mond, J.J., Prince, G. and Klinman, D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 99 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)

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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCCCGATGCAGGGGG 18
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LOCUS AX465432 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 100 from Patent WO0211761.
ACCESSION AX465432
VERSION AX465432.1 GI:21899795
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mond, J.J., Prince, G. and Klinman, D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 100 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)

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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 13
AX352224
LOCUS AX352224 28 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 520 from Patent WO0193902.
ACCESSION AX352224
VERSION AX352224.1 GI:18617507
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 520 13-DEC-2001;
Biosynexus Incorporated (US)

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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCCCGATGCAGGGGG 18
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Db 3 TCGTCGATGCAGGGGG 20

RESULT 13
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LOCUS AX352224 28 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 520 from Patent WO0193902.
ACCESSION AX352224
VERSION AX352224.1 GI:18617507
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 520 13-DEC-2001;
Biosynexus Incorporated (US)

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ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 28;
Best Local Similarity 94.4%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCCCGATGCAGGGGG 18
||| ||||| ||||| |||||
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RESULT 14
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LOCUS AX352236 28 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 532 from Patent WO0193902.
ACCESSION AX352236
VERSION AX352236.1 GI:18617519
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 532 13-DEC-2001;
Biosynexus Incorporated (US)

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Query Match 91.1%; Score 16.4; DB 6; Length 28;
Best Local Similarity 94.4%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCCCGATGCAGGGGG 18
||| ||||| ||||| |||||
Db 11 TGCACGATGCAGGGGG 28

RESULT 15

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AE012163
LOCUS
DEFINITION
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of 460 of the complete genome.
ACCESSION
VERSION
AB012163.1 GI:21111651
KEYWORDS
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Xanthomonas campestris pv. campestris str. ATCC 33913
Xanthomonas campestris pv. campestris str. ATCC 33913
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
1 (bases 1 to 13936)
da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Farah, C.S., Furlan, L.R.,
Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida
Jr., N.F., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C.,
Camargo, L.B.A., Camarotte, G., Cannavan, F., Cardozo, J.,
Chambergo, F., Cispina, L.P., Cicarelli, R.M.B., Coutinho, L.L.,
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Ferreira, R.C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C.,
Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite
Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A.,
Madeira, A.M.B.N., Martinez-Rossi, N.M., Martins, E.C., Meidanis, J.,
Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, I.M., Novo, M.T.M.,
Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira Jr., H.A.,
Rosa, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F.,
Takita, M.A., Tamura, R.E., Teixeira, E.C., Tezza, R.I.D., Trindade dos
Santos, M., Truffi, D., Tsai, S.M., White, F.P., Setubal, J.C. and
Kitajima, J.P.
Comparison of the genomes of two Xanthomonas pathogens with
differing host specificities
Nature 417 (6887), 459-463 (2002)
2022145
PUBMED
12024217
2 (bases 1 to 13936)
da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Farah, C.S., Furlan, L.R.,
Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida
Jr., N.F., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C.,
Camargo, L.B.A., Camarotte, G., Cannavan, F., Cardozo, J.,
Chambergo, F., Cispina, L.P., Cicarelli, R.M.B., Coutinho, L.L.,
Curisno-Santos, J.R., El-Dorry, H., Faria, J.B., Ferreira, A.J.S.,
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Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite
Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A.,
Madeira, A.M.B.N., Martinez-Rossi, N.M., Martins, E.C., Meidanis, J.,
Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, I.M., Novo, M.T.M.,
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Santos, M., Truffi, D., Tsai, S.M., White, F.P., Setubal, J.C. and
Kitajima, J.P.
Direct Submission
Submitted (28-NOV-2001) Departamento de Bioquímica, Universidade de
Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900,
Brazil
FEATURES
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Best Local Similarity 94.4%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  TCGCGCATGCGAGGGGG 18
      |||||
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Job time : 636.732 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 06:05:50 ; Search time 134.89 Seconds
(without alignments)
566.887 Million cell updates/sec

Title: US-10-068-160-18

Perfect score: 18

Sequence: 1 tgcgcccagtcagggggg 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

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Listing first 45 summaries

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4: Geneseqn2001as:*

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6: Geneseqn2002as:*

7: Geneseqn2003as:*

8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	20	7	ACC48303 CpG oligo
2	17	94.4	19	4	AAC80656 Immunogen
3	17	94.4	19	4	AAS09626 Immunorea
4	17	94.4	19	6	ABK46504 Immunosti
5	16.4	91.1	20	4	AAC80662 Immunogen
6	16.4	91.1	20	4	AAC80661 Immunogen
7	16.4	91.1	20	4	AAC80620 Immunogen
8	16.4	91.1	20	4	AAS09631 Immunorea
9	16.4	91.1	20	4	AAS09590 Immunorea
10	16.4	91.1	20	4	AAS09651 Immunorea
11	16.4	91.1	20	4	AAS09632 Immunorea
12	16.4	91.1	20	6	ABL35573 Immunosti
13	16.4	91.1	20	6	ABL35584 Immunosti
14	16.4	91.1	20	6	ABL35617 Immunosti
15	16.4	91.1	20	6	ABK46510 Immunosti
16	16.4	91.1	20	6	ABK46468 Immunosti
17	16.4	91.1	20	6	ABK46509 Immunosti
18	16.4	91.1	20	7	ACC48311 CpG oligo
19	16.4	91.1	20	7	ACC48298 CpG oligo
20	16.4	91.1	20	7	ACC48312 CpG oligo
21	16.4	91.1	20	7	ACC48306 CpG oligo
22	16.4	91.1	20	7	ACC48319 CpG oligo
23	16.4	91.1	20	8	ACC83116 D class C

24	16.4	91.1	20	8	ACC83117 D class C
25	16.4	91.1	20	8	ACC83124 D class C
26	16.4	91.1	20	9	ADD01050 CpG D oli
27	16.4	91.1	20	9	ADD01059 CpG D oli
28	16.4	91.1	28	6	ABL35594 Immunosti
29	16.4	91.1	28	6	ABL35606 Immunosti
30	15.4	85.6	19	4	AAC80602 Immunogen
31	15.4	85.6	19	4	AAC80663 Immunogen
32	15.4	85.6	19	4	AAS09633 Immunorea
33	15.4	85.6	19	4	AAS09572 Immunorea
34	15.4	85.6	19	6	ABK46450 Immunosti
35	15.4	85.6	19	6	ABK46511 Immunosti
c	36	15.4	675	6	AAS62113 Porcine m
37	15.4	85.6	682	5	AAS77915 DNA encod
38	15.4	85.6	755	3	AAL13360 Aspergill
c	39	15.4	759	9	AD62051 Rat gene
c	40	15.4	759	9	AD62051 Rat gene
41	15	83.3	2712	7	ACA26785 Prokaryot
42	14.8	82.2	18	6	ABL35587 Immunosti
43	14.8	82.2	18	6	ABL35577 Immunosti
44	14.8	82.2	18	6	ABL35625 Immunosti
45	14.8	82.2	18	9	ADD01052 CpG D oli

ALIGNMENTS

RESULT 1

ACC48303 standard; DNA; 20 BP.

XX AC ACC48303;

XX AC ACC48303;

DT 11-AUG-2003 (first entry)

XX CpG oligodeoxynucleotide used for dendritic cell maturation.

DB CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;

XX CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;

KW cytosstatic; immunostimulant; gene therapy; ss.

XX Synthetic.

OS Synthetic.

XX Key

PH Location/Qualifiers

FT misc_difference 1

FT /tag= a

FT /note= "N is any base (especially G) or no base"

FT misc_difference 2

FT /tag= b

FT /note= "N is any base (especially G) or no base"

XX WO2003020884-A2.

XX 13-MAR-2003.

XX 13-AUG-2002; 2002WO-US025732.

XX 14-AUG-2001; 2001US-0312190P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Klinman DM, Gursel M, Verthelyi D;

XX WPI; 2003-300874/29.

XX Generating mature dendritic cells for tumor immunotherapy or as vaccines

XX for activating the immune system to treat diseases such as cancer,

XX comprises contacting a dendritic cell precursor with a D type

XX oligodeoxynucleotide.

XX Disclosure; Page 26; 69pp; English.

XX The present sequence is that of a D type CpG oligodeoxynucleotide that is

XX an example of claimed D type oligodeoxynucleotides (see ACC48294) of the

CC invention. Mature dendritic cells are obtained by contacting a dendritic
 CC cell precursor, such as a monocyte, with such an oligodeoxynucleotide.
 CC The method is useful for generating mature dendritic cells and enhancing
 CC T cell responses, thus enhancing antigen presentation. Mature dendritic
 CC cells are useful for tumour immunotherapy, for augmenting an immune
 CC response to an infectious agent or to a vaccine, and as vaccines to
 CC prevent future infection or to activate the immune system to treat
 CC diseases such as cancer. Mature dendritic cells may also be used to
 CC produce activated T lymphocytes

XX
 SQ Sequence 20 BP; 2 A; 4 C; 10 G; 2 T; 0 U; 2 Other;
 Query Match 100.0%; Score 18; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCCGATGACGGGG 18
 |||||
 Db 3 TCGCCGATGACGGGG 20
 |||||

RESULT 2
 AAC80656
 ID AAC80656 standard; DNA; 19 BP.
 AC AAC80656;
 XX
 DT 14-FEB-2001 (first entry)
 DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:76.
 XX

CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
 immunogenic; cytokine release; natural killer cell; NK cell activation;
 cell-mediated immune response; T-cell response; humoral response;
 B-cell response; antibody production; immune response induction; vaccine;
 allergy; asthma; infection; bacterial; viral; fungal; protozoal;
 parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
 rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
 immune deficiency; biological warfare agent; cytostatic; antiarthritic;
 antimicrobial; antiallergic; protozoicide; tuberculostatic;
 antiasthmatic; dermatological; phosphorothioate; ss.
 Synthetic.
 OS
 XX
 PN WO200061151-A2.
 XX
 XX
 PD 19-OCT-2000.
 XX
 PF 12-APR-2000; 2000WO-US009839.
 XX
 PR 12-APR-1999; 99US-0128898P.
 XX
 XX (KLIN/) KLINMAN D.
 PA (ISHI/) ISHII K.
 PA (VERT/) VERTHELYI D.
 XX
 PI Klinman D, Ishii K, Verthelyi D;
 DR WPI; 2001-006880/01.
 XX
 XX Novel oligonucleotides useful for the prevention and treatment of
 PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
 PT resulting from exposure to a bio-warfare agent.
 XX
 XX
 PS Claim 4; Page 35; 46pp; English.
 XX
 XX The invention relates to novel immunogenic CpG oligodeoxynucleotides
 CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
 CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
 CC optionally have phosphorothioate linkages which make them more resistant
 CC to degradation. The invention also relates to an oligonucleotide delivery
 CC complex comprising an oligonucleotide of the invention and a targeting

CC agent, and a pharmaceutical composition comprising the oligonucleotide
 CC delivery complex. The oligonucleotides are able to induce either a cell-
 CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 CC oligonucleotides of the sequence 5'-RY-CpG-RY-3', being able to induce a
 CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3',
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g. macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergenic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic
 CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antisense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention

XX
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 Query Match 94.4%; Score 17; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCCGATGACGGGG 17
 |||||
 Db 3 TCGCCGATGACGGGG 19
 |||||

RESULT 3
 AAS09626
 ID AAS09626 standard; DNA; 19 BP.
 XX
 AC AAS09626;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Immunoreactive CpG sequence-containing oligonucleotide #76.
 XX

CpG sequence; immune response; non-B cell activation; interferon gamma;
 IFN-gamma; humoral; antibody production; interleukin-6 production;
 therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 Leishmania; Ebola; Anthrax; Listeria; ss.
 Synthetic.
 OS
 XX
 PN WO200151500-A1.
 XX
 PD 19-JUL-2001.
 XX
 PF 12-JAN-2001; 2001WO-US001122.
 XX
 PR 14-JAN-2000; 2000US-0176115P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

```

XX Klinman D, Ishii K, Verthelyi D;
XX WPI; 2001-442129/47.
XX
XX Oligodeoxynucleotides for inducing an immune response to treat and
XX prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
XX resulting from exposure to bio-warfare agents, comprise multiple CpG
XX sequences.
XX
XX Claim 5; Page 39; 48pp; English.
XX
XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
XX nucleotides comprising multiple CpG sequences, where one of the CpG
XX sequences is different from another of the multiple CpG sequences. The
XX ODN are useful for inducing an immune response, preferably a cell-
XX mediated immune response, involving non-B cell activation, interferon
XX gamma (IFN-gamma) production or a humoral immune response involving B
XX cell activation, antibody and interleukin-6 production in a host, for
XX treating, preventing or ameliorating an allergic reaction, e.g. asthma,
XX cancer, e.g. solid tumour cancer, a disease associated with the immune
XX system e.g. autoimmune disorder or an immune system deficiency, infection
XX or a symptom resulting from exposure to bio-warfare agent in a human. The
XX induction of immune response improves the efficacy of a vaccine and is
XX used in antisense therapy. The ODN are useful for treating, preventing or
XX ameliorating allergic reactions, including eczema, allergic rhinitis or
XX coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
XX and other atopic conditions, for improving the efficacy of vaccines
XX against hepatitis A, B and C, human immunodeficiency virus (HIV) and
XX malaria, for treating immune system deficiencies, e.g. lupus
XX erythematosus and autoimmune diseases such as rheumatoid arthritis and
XX multiple sclerosis, infections including Francisella, schistosomiasis,
XX tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
XX symptoms resulting from exposure of bio-warfare agent, including Ebola,
XX Anthrax and Listeria
XX
XX Sequence 19 BP; 2 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 94.4%; Score 17; DB 4; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX QY 1 TGGCCCGATGCAGGGGG 17
XX |||||
XX Db 3 TGGCCCGATGCAGGGGG 19
XX
XX RESULT 4
XX ABK46504
XX ID ABK46504 standard; DNA; 19 BP.
XX AC ABK46504;
XX
XX 05-JUN-2002 (first entry)
XX
XX Immunostimulatory unmethylated CpG oligodeoxynucleotide #94.
XX
XX unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine;
XX Paramyxoviridae; F protein; respiratory syncytial virus; RSV;
XX viral bronchiolitis; pneumonia; infectious pulmonary disease;
XX bronchopulmonary dysplasia; congenital heart condition; ss.
XX
XX Synthetic.
XX
XX WO200211761-A2.
XX
XX 14-FEB-2002.
XX
XX 09-AUG-2001; 2001WO-US041633.
XX
XX 10-AUG-2000; 2000US-0224011P.
XX
XX 01-SEP-2000; 2000US-0229307P.
XX

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XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX Mond JJ, Prince G, Klinman DM;
XX WPI; 2002-227118/28.
XX
XX Vaccine for immunizing patient against respiratory syncytial virus, has
XX epitopes of Paramyxoviridae F protein, and cytosine followed by guanine
XX linked by phosphate bond-oligodeoxynucleotides.
XX
XX Claim 4; Page 9; 30pp; English.
XX
XX The invention describes a vaccine comprising one or more epitopes of a
XX Paramyxoviridae F protein, and one or more CpG (cytosine followed by
XX guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The
XX vaccine is useful for vaccinating a patient especially against viruses of
XX the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the
XX primary cause of viral bronchiolitis and pneumonia in infants and
XX children, and infectious pulmonary disease in infants. RSV has been
XX particularly implicated in death of infants that are premature, have
XX bronchopulmonary dysplasia, or congenital heart conditions. This sequence
XX represents an oligodeoxynucleotide that can be used in the creation of
XX the vaccine
XX
XX Sequence 19 BP; 2 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 94.4%; Score 17; DB 6; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TGGCCCGATGCAGGGGG 17
XX |||||
XX Db 3 TGGCCCGATGCAGGGGG 19
XX
XX RESULT 5
XX AAC80662
XX ID AAC80662 standard; DNA; 20 BP.
XX AC AAC80662;
XX
XX 14-FEB-2001 (first entry)
XX
XX Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:82.
XX
XX CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
XX immunogenic; cytokine release; natural killer cell; NK cell activation;
XX cell-mediated immune response; T-cell response; humoral response; vaccine;
XX B-cell response; antibody production; immune response induction; protozoal;
XX allergy; asthma; infection; bacterial; viral; fungal; protozoal;
XX parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
XX rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
XX immune deficiency; biological warfare agent; cytostatic; antiarthritic;
XX antimicrobial; antiallergic; protozoacide; tuberculostatic;
XX antiasthmatic; dermatological; phosphorothioate; ss.
XX
XX Synthetic.
XX
XX WO2000061151-A2.
XX
XX 19-OCT-2000.
XX
XX 12-APR-2000; 2000WO-US009839.
XX
XX 12-APR-1999; 99US-0128898P.
XX
XX (KLIN/) KLINMAN D.
XX (ISHI/) ISHII K.
XX (VERT/) VERTHELYI D.
XX
XX Klinman D, Ishii K, Verthelyi D;
XX WPI; 2001-006880/01.
XX

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XX Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.

XX Claim 4; Page 36; 46pp; English.

XX The invention relates to novel immunogenic CpG oligodeoxynucleotides
XX (AAC80581-C80723). The oligonucleotides are at least 10 bases long and
XX comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
XX -3'. The central CpG motif is unmethylated, and the oligonucleotides
XX optionally have phosphorothioate linkages which make them more resistant
XX to degradation. The invention also relates to an oligonucleotide delivery
XX complex comprising an oligonucleotide of the invention and a targeting
XX agent, and a pharmaceutical composition comprising the oligonucleotide
XX delivery complex. The oligonucleotides are able to induce either a cell-
XX mediated (T-cell) response or a humoral (B-cell, antibody) response, with
XX oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
XX cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
XX being able to induce a humoral response. It is thought that after
XX administration, the oligonucleotide acts on antigen-presenting cells
XX (e.g., macrophages and dendritic cells), which then release cytokines,
XX leading to activation of natural killer (NK) cells. A cell-mediated or
XX humoral response can then occur by activation of T- or B-cells. The
XX induction of an immune response is useful for treating, preventing or
XX ameliorating an allergic reaction (preferably asthma), or an infection,
XX where an immunogenic CpG oligonucleotide is administered either alone or
XX in combination with an anti-allergenic agent or anti-infectious agent.
XX The allergic conditions which may be treated include eczema, allergic
XX rhinitis, hayfever, urticaria, food allergies and other atopic
XX conditions, and the infections which may be treated include viral,
XX bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
XX leishmania and schistosomiasis. Immune response induction may also be
XX used in the treatment of an autoimmune disorder (e.g., lupus
XX erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
XX associated with immune system deficiency, and symptoms resulting from
XX exposure to an agent of biological warfare. An immunogenic CpG
XX oligonucleotide, either alone or in combination with an anti-cancer
XX agent, is useful for treating solid tumour cancer. The induction of an
XX immune response is used in antisense therapy and to improve the efficacy
XX of a vaccine. The oligonucleotide is preferably administered to
XX lymphocytes ex vivo, producing activated lymphocytes which are then
XX administered to the host. The present sequence represents an immunogenic
XX CpG oligodeoxynucleotide of the invention

XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 20;

Best Local Similarity 94.4%; Pred. No. 2.2e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCGATGACGGGGG 18

DB 3 TGGCGTCGATGACGGGGG 20

RESULT 6

AAC80661

ID AAC80661 standard; DNA; 20 BP.

AC AAC80661;

XX 14-FEB-2001 (first entry)

XX Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:81.

XX CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;

XX immunogenic; cytokine release; natural killer cell; NK cell activation;

XX cell-mediated immune response; T-cell response; humoral response;

XX B-cell response; antibody production; immune response induction; vaccine;

XX allergy; asthma; infection; bacterial; viral; fungal; protozoal;

XX parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;

XX rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;

KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; anti-allergic; protozoic; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.

OS Synthetic.

XX WO200061151-A2.

XX 19-OCT-2000.

XX 12-APR-2000; 2000WO-US009839.

XX 12-APR-1999; 99US-0128898P.

XX {KLIN//} KLINMAN D.

XX {ISHI//} ISHII K.

XX {VERT//} VERTHELYI D.

XX Klinman D. Ishii K. Verthelyi D.

XX WPI; 2001-006880/01.

XX Novel oligonucleotides useful for the prevention and treatment of

XX allergies, cancer, and autoimmune disorders and for ameliorating symptoms

XX resulting from exposure to a bio-warfare agent.

XX Claim 4; Page 36; 46pp; English.

XX The invention relates to novel immunogenic CpG oligodeoxynucleotides
XX (AAC80581-C80723). The oligonucleotides are at least 10 bases long and
XX comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
XX -3'. The central CpG motif is unmethylated, and the oligonucleotides
XX optionally have phosphorothioate linkages which make them more resistant
XX to degradation. The invention also relates to an oligonucleotide delivery
XX complex comprising an oligonucleotide of the invention and a targeting
XX agent, and a pharmaceutical composition comprising the oligonucleotide
XX delivery complex. The oligonucleotides are able to induce either a cell-
XX mediated (T-cell) response or a humoral (B-cell, antibody) response, with
XX oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
XX cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
XX being able to induce a humoral response. It is thought that after
XX administration, the oligonucleotide acts on antigen-presenting cells
XX (e.g., macrophages and dendritic cells), which then release cytokines,
XX leading to activation of natural killer (NK) cells. A cell-mediated or
XX humoral response can then occur by activation of T- or B-cells. The
XX induction of an immune response is useful for treating, preventing or
XX ameliorating an allergic reaction (preferably asthma), or an infection,
XX where an immunogenic CpG oligonucleotide is administered either alone or
XX in combination with an anti-allergenic agent or anti-infectious agent.
XX The allergic conditions which may be treated include eczema, allergic
XX rhinitis, hayfever, urticaria, food allergies and other atopic
XX conditions, and the infections which may be treated include viral,
XX bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
XX leishmania and schistosomiasis. Immune response induction may also be
XX used in the treatment of an autoimmune disorder (e.g., lupus
XX erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
XX associated with immune system deficiency, and symptoms resulting from
XX exposure to an agent of biological warfare. An immunogenic CpG
XX oligonucleotide, either alone or in combination with an anti-cancer
XX agent, is useful for treating solid tumour cancer. The induction of an
XX immune response is used in antisense therapy and to improve the efficacy
XX of a vaccine. The oligonucleotide is preferably administered to
XX lymphocytes ex vivo, producing activated lymphocytes which are then
XX administered to the host. The present sequence represents an immunogenic
XX CpG oligodeoxynucleotide of the invention

XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 20;

Best Local Similarity 94.4%; Pred. No. 2.2e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCGATGACGGGGG 18

DB 3 TGGCGTCGATGACGGGGG 20

RESULT 6

AAC80661

ID AAC80661 standard; DNA; 20 BP.

AC AAC80661;

XX 14-FEB-2001 (first entry)

XX Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:81.

XX CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;

XX immunogenic; cytokine release; natural killer cell; NK cell activation;

XX cell-mediated immune response; T-cell response; humoral response;

XX B-cell response; antibody production; immune response induction; vaccine;

XX allergy; asthma; infection; bacterial; viral; fungal; protozoal;

XX parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;

XX rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;

Query Match 91.1%; Score 16.4; DB 4; Length 20;

Best Local Similarity 94.4%; Pred. No. 2.2e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCGATGACGGGGG 18

Db 3 TGGCTCGATGCAGGGGG 20
 RESULT 7
 AAC80620
 ID AAC80620 standard; DNA; 20 BP.
 XX AAC80620;
 AC AAC80620;
 XX
 DT 14-FEB-2001 (first entry)
 XX
 DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:40.
 XX
 KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
 KW immunogenic; cytokine release; natural killer cell; NK cell activation;
 KW cell-mediated immune response; T-cell response; humoral response;
 KW B-cell response; antibody production; immune response induction; vaccine;
 KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
 KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
 KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
 KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
 KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
 KW antiasthmatic; dermatological; phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 WO200061151-A2.
 XX
 PN 19-OCT-2000.
 XX
 PD
 XX
 PF 12-APR-2000; 2000WO-US009839.
 XX
 PR 12-APR-1999; 99US-0128898P.
 XX
 PA (KLIN/) KLINMAN D.
 PA (ISHI/) ISHII K.
 PA (VERT/) VERTHELYI D.
 XX
 PI Klinman D, Ishii K, Verthelyi D;
 XX
 DR WPI; 2001-006880/01.
 XX
 PT Novel oligonucleotides useful for the prevention and treatment of
 PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
 PT resulting from exposure to a bio-warfare agent.
 XX
 FS Claim 4; Page 30; 45pp; English.
 XX
 CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
 CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
 CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
 CC optionally have phosphorothioate linkages which make them more resistant
 CC to degradation. The invention also relates to an oligonucleotide delivery
 CC complex comprising an oligonucleotide of the invention and a targeting
 CC agent, and a pharmaceutical composition comprising the oligonucleotide
 CC delivery complex. The oligonucleotides are able to induce either a cell-
 CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
 CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3',
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g., macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergenic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic
 CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antisense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention
 XX
 SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 91.1%; Score 16.4; DB 4; Length 20;
 Best Local Similarity 94.4%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGGCTCGATGCAGGGGG 18
 Db 3 TGGCTCGATGCAGGGGG 20
 RESULT 8
 AAS09631
 ID AAS09631 standard; DNA; 20 BP.
 XX
 AC AAS09631;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Immunoreactive CpG sequence-containing oligonucleotide #81.
 XX
 KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW leishmania; Ebola; Anthrax; Listeria; ss.
 XX
 OS Synthetic.
 XX
 WO200151500-A1.
 XX
 PN 19-JUL-2001.
 XX
 PD 12-JAN-2001; 2001WO-US001122.
 XX
 PF 14-JAN-2000; 2000US-0176115P.
 XX
 PR (USSH) US DBPT HEALTH & HUMAN SERVICES.
 PA
 XX Klinman D, Ishii K, Verthelyi D;
 XX
 DR WPI; 2001-442129/47.
 XX
 PT Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.
 XX
 FS Claim 5; Page 40; 48pp; English.
 XX
 CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon

CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria
 XX
 SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 91.1%; Score 16.4; DB 4; Length 20;
 Best Local Similarity 94.4%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TCGCCGATGCGAGGGGG 18
 DB 3 TCGTCGATGCGAGGGGG 20
 RESULT 9
 AAS09590
 ID AAS09590 standard; DNA; 20 BP.
 AC AAS09590;
 XX
 XX 26-SEP-2001 (first entry)
 XX Immunoreactive CpG sequence-containing oligonucleotide #40.
 XX
 KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.
 OS Synthetic.
 XX
 XX WO200151500-A1.
 PN
 PD 19-JUL-2001.
 XX
 XX 12-JAN-2001; 2001WO-US001122.
 PF
 XX
 PR 14-JAN-2000; 2000US-0176115P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Klinman D, Ishii K, Verthelyi D;
 FI
 XX WPI; 2001-442129/47.
 DR
 XX
 XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.
 XX
 XX Claim 5; Page 33; 48pp; English.

CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria
 XX
 SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 91.1%; Score 16.4; DB 4; Length 20;
 Best Local Similarity 94.4%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TCGCCGATGCGAGGGGG 18
 DB 3 TCGTCGATGCGAGGGGG 20
 RESULT 10
 AAS09651
 ID AAS09651 standard; DNA; 20 BP.
 AC AAS09651;
 XX
 XX 26-SEP-2001 (first entry)
 XX Immunoreactive CpG sequence-containing oligonucleotide #101.
 XX
 KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.
 OS Synthetic.
 XX
 XX WO200151500-A1.
 PN
 PD 19-JUL-2001.
 XX
 XX 12-JAN-2001; 2001WO-US001122.
 PF
 XX
 PR 14-JAN-2000; 2000US-0176115P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Klinman D, Ishii K, Verthelyi D;
 FI
 XX WPI; 2001-442129/47.
 DR
 XX
 XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms

PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
XX
PS Claim 5; Page 44; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCGCGATCGAGGGGG 18
||| ||||| ||||| |||||
Db 3 TGCACCGATCGAGGGGG 20

RESULT 11
ID AAS09632
AC AAS09632;
XX
XX 26-SEP-2001 (first entry)
DE
DE Immunoreactive CpG sequence-containing oligonucleotide #82.
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
XX WO200151500-A1.
XX
XX 19-JUL-2001.
XX
XX 12-JAN-2001; 2001WO-US001122.
XX
XX 14-JAN-2000; 2000US-0176115P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Klinman D, Ishii K, Verthelyi D;

XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
XX
PS Claim 5; Page 40; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
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CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCGCGATCGAGGGGG 18
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Db 3 TGGCTCGATCGAGGGGG 20

RESULT 12
ID ABL35573
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XX ABL35573 standard; DNA; 20 BP.
XX
XX ABL35573;
XX
XX 04-APR-2002 (first entry)
XX
XX Immunostimulatory oligonucleotide SEQ ID NO: 499.
KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW infection; allergy; cancer; hypersensitivity; bio-warfare;
KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW antiinflammatory; antibacterial; ss.
XX
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
XX misc_RNA 1..20
XX /+tag= a
XX /note= "optionally thymidine is replaced by uracil to
XX form RNA or DNA/RNA hybrids. Thymidine is linked to at
XX least one other base through a ribose sugar"
XX
XX WO200193902-A2.
XX
XX 13-DEC-2001.

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XX 07-JUN-2001; 2001WO-US018276.
XX
XX 07-JUN-2000; 2000US-0209797P.
XX
XX (BIOS-) BIOSYNEXUS INC.
XX
XX Mond JJ, Flora M, Klinman DM;
XX
XX WPI; 2002-130570/17.
XX
XX New immunostimulatory compositions comprising RNA/DNA hybrid
XX oligonucleotides, useful for enhancing an immune response or inducing
XX cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX HIV infection.
XX
XX Example 11; Page 61; 68pp; English.
XX
XX The present invention relates to an immunostimulatory composition, which
XX comprises at least one oligonucleotide comprising both an RNA region and
XX a DNA region. The composition is useful for enhancing an immune response
XX or inducing cytokines. It can be used as a vaccine adjuvant and in
XX treating diseases, including pathogenic infection, (non-)malignant
XX tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX hepatitis, HIV or malaria. The composition is also useful for treating,
XX preventing or ameliorating the symptoms resulting from exposure to a bio-
XX warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX an immunostimulatory oligonucleotide described in the exemplification of
XX the invention
XX
XX Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 91.1%; Score 16.4; DB 6; Length 20;
XX Best Local Similarity 94.4%; Pred. No. 2.2e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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XX QY 1 TGCGCCGATGCAGGGGG 18
XX |||||
XX Db 3 TGCACCGATGCAGGGGG 20
XX
XX RESULT 13
XX ABL35584
XX ID ABL35584 standard; DNA; 20 BP.
XX
XX AC ABL35584;
XX
XX DT 04-APR-2002 (first entry)
XX
XX DE Immunostimulatory oligonucleotide SEQ ID NO: 510.
XX
XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX infection; allergy; cancer; hypersensitivity; bio-warfare;
XX immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX immunosuppressive; protozoicide; virucide; hepatotropic; gene therapy;
XX antiinflammatory; antibacterial; ss.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX Key misc_RNA 1..20
XX /tag= a
XX /note= "optionally thymidine is replaced by uracil to
XX form RNA or DNA/RNA hybrids. Thymidine is linked to at
XX least one other base through a ribose sugar"
XX
XX WO200193902-A2.
XX
XX 13-DEC-2001.
XX
XX 07-JUN-2001; 2001WO-US018276.
XX
XX PF

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XX 07-JUN-2000; 2000US-0209797P.
XX
XX (BIOS-) BIOSYNEXUS INC.
XX
XX Mond JJ, Flora M, Klinman DM;
XX
XX WPI; 2002-130570/17.
XX
XX New immunostimulatory compositions comprising RNA/DNA hybrid
XX oligonucleotides, useful for enhancing an immune response or inducing
XX cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX HIV infection.
XX
XX Example 11; Page 61; 68pp; English.
XX
XX The present invention relates to an immunostimulatory composition, which
XX comprises at least one oligonucleotide comprising both an RNA region and
XX a DNA region. The composition is useful for enhancing an immune response
XX or inducing cytokines. It can be used as a vaccine adjuvant and in
XX treating diseases, including pathogenic infection, (non-)malignant
XX tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX hepatitis, HIV or malaria. The composition is also useful for treating,
XX preventing or ameliorating the symptoms resulting from exposure to a bio-
XX warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX an immunostimulatory oligonucleotide described in the exemplification of
XX the invention
XX
XX Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 91.1%; Score 16.4; DB 6; Length 20;
XX Best Local Similarity 94.4%; Pred. No. 2.2e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 TGCGCCGATGCAGGGGG 18
XX |||||
XX Db 3 TGCACCGATGCAGGGGG 20
XX
XX RESULT 14
XX ABL35617
XX ID ABL35617 standard; DNA; 20 BP.
XX
XX AC ABL35617;
XX
XX DT 04-APR-2002 (first entry)
XX
XX DE Immunostimulatory oligonucleotide SEQ ID NO: 543.
XX
XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX infection; allergy; cancer; hypersensitivity; bio-warfare;
XX immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX immunosuppressive; protozoicide; virucide; hepatotropic; gene therapy;
XX antiinflammatory; antibacterial; ss.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX Key misc_RNA 1..20
XX /tag= a
XX /note= "optionally thymidine is replaced by uracil to
XX form RNA or DNA/RNA hybrids. Thymidine is linked to at
XX least one other base through a ribose sugar"
XX
XX WO200193902-A2.
XX
XX 13-DEC-2001.
XX
XX 07-JUN-2001; 2001WO-US018276.
XX
XX PF
XX 07-JUN-2000; 2000US-0209797P.
XX
XX PF

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XX PA (BIOS-) BIOSNEXUS INC.
 XX PI Mond JJ, Flora M, Klinman DM;
 XX DR WPI; 2002-130570/17.
 XX PT New immunostimulatory compositions comprising RNA/DNA hybrid
 PT oligonucleotides, useful for enhancing an immune response or inducing
 PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
 PT HIV infection.
 XX PS Example 11; Page 62; 68pp; English.
 XX CC The present invention relates to an immunostimulatory composition, which
 CC comprises at least one oligonucleotide comprising both an RNA region and
 CC a DNA region. The composition is useful for enhancing an immune response
 CC or inducing cytokines. It can be used as a vaccine adjuvant and in
 CC treating diseases, including pathogenic infection, (non-)malignant
 CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
 CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
 CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
 CC hepatitis, HIV or malaria. The composition is also useful for treating,
 CC preventing or ameliorating the symptoms resulting from exposure to a bio-
 CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
 CC an immunostimulatory oligonucleotide described in the exemplification of
 CC the invention
 XX SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
 Query Match 91.1%; Score 16.4; DB 6; Length 20;
 Best Local Similarity 94.4%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 TGGCCCGATGCAGGGGG 18
 Db 3 TGCACCGATGCAGGGGG 20
 Search completed: July 2, 2004, 08:31:38
 Job time : 134.89 secs

PT linked by phosphate bond-oligodideoxynucleotides.
 XX Claim 4; Page 9; 30pp; English.
 XX CC The invention describes a vaccine comprising one or more epitopes of a
 CC Paramyxoviridae F protein, and one or more CpG (cytosine followed by
 CC guanine linked by phosphate bond)-oligodideoxynucleotides (ODNs). The
 CC vaccine is useful for vaccinating a patient especially against viruses of
 CC the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the
 CC primary cause of viral bronchiolitis and pneumonia in infants and
 CC children, and infectious pulmonary disease in infants. RSV has been
 CC particularly implicated in death of infants that are premature, have
 CC bronchopulmonary dysplasia, or congenital heart conditions. This sequence
 CC represents an oligodideoxynucleotide that can be used in the creation of
 CC the vaccine
 XX SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 91.1%; Score 16.4; DB 6; Length 20;
 Best Local Similarity 94.4%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 TGGCCCGATGCAGGGGG 18
 Db 3 TGCACCGATGCAGGGGG 20
 Search completed: July 2, 2004, 08:31:38
 Job time : 134.89 secs

RESULT 15
 ID ABK46510
 XX ABK46510 standard; DNA; 20 BP.
 XX AC ABK46510;
 XX DF 05-JUN-2002 (first entry)
 XX DE Immunostimulatory unmethylated CpG oligodideoxynucleotide #100.
 XX KM unmethylated CpG; oligodideoxynucleotide; ODN; virucide; vaccine;
 XX KW Paramyxoviridae; F protein; respiratory syncytial virus; RSV;
 KW viral bronchiolitis; pneumonia; infectious pulmonary disease;
 KW bronchopulmonary dysplasia; congenital heart condition; ss.
 XX OS Synthetic.
 XX PN WO200211761-A2.
 XX PD 14-FEB-2002.
 XX PF 09-AUG-2001; 2001WO-US041633.
 XX PR 10-AUG-2000; 2000US-0224011P.
 PR 01-SEP-2000; 2000US-0229307P.
 XX PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
 XX PI Mond JJ, Prince G, Klinman DM;
 XX WPI; 2002-227118/28.
 XX PT Vaccine for immunizing patient against respiratory syncytial virus, has
 PT epitopes of Paramyxoviridae F protein, and cytosine followed by guanine

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:09:30 ; Search time 28.2073 Seconds
(without alignments)
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Title: US-10-068-160-18

Sequence: 1 tgcgcgatgcaggggg 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 5: /cgn2_6/prodata/2/ina/6C COMB.seq:*
- 6: /cgn2_6/prodata/2/ina/6D COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.8	82.2	3358	3	US-09-248-571-2
2	14.8	82.2	3358	4	US-09-553-736-2
3	14.8	82.2	3728	1	US-08-111-939-1
4	14.8	82.2	10380	3	US-09-077-354B-3
5	14.8	82.2	33529	3	US-09-144-085-3
6	14.8	82.2	4403765	3	US-09-103-840A-2
7	14.8	82.2	441529	3	US-09-103-840A-1
8	14.4	80.0	648	4	US-09-252-991A-4236
9	14.4	80.0	756	3	US-09-175-014-1
10	14.4	80.0	771	4	US-09-252-991A-4440
11	14.4	80.0	1024	4	US-09-328-475C-59
12	14.4	80.0	1488	4	US-09-252-991A-4168
13	14.4	80.0	1503	4	US-09-252-991A-4543
14	14.4	80.0	2870	4	US-09-799-875-16
15	14.4	80.0	2891	4	US-09-578-441-1
16	14.4	77.8	519	4	US-09-252-991A-2220
17	14.4	77.8	615	4	US-09-252-991A-5794
18	14.4	77.8	879	4	US-09-252-991A-2380
19	14.4	77.8	1407	4	US-09-252-991A-2455
20	14.4	77.8	1617	4	US-09-252-991A-5856
21	14.4	77.8	2019	4	US-09-252-991A-5836
22	14.4	77.8	2391	4	US-09-252-991A-5912
23	14.4	77.8	2814	4	US-09-252-991A-2537
24	13.8	76.7	20	4	US-09-659-845A-106
25	13.8	76.7	236	4	US-09-621-976-18710
26	13.8	76.7	382	4	US-09-833-381-178
27	13.8	76.7	462	4	US-09-252-991A-9628

28	13.8	76.7	468	4	US-09-252-991A-9670	Sequence 9670, Ap
29	13.8	76.7	594	4	US-09-489-039A-7023	Sequence 7023, Ap
30	13.8	76.7	597	4	US-09-252-991A-14469	Sequence 14469, A
31	13.8	76.7	630	4	US-09-489-039A-9630	Sequence 9630, Ap
32	13.8	76.7	633	4	US-09-489-039A-2752	Sequence 2752, Ap
33	13.8	76.7	699	4	US-09-252-991A-11367	Sequence 11367, A
34	13.8	76.7	885	4	US-09-252-991A-7532	Sequence 7532, Ap
35	13.8	76.7	912	4	US-09-252-991A-7811	Sequence 7811, Ap
36	13.8	76.7	1011	4	US-09-252-991A-9228	Sequence 9228, Ap
37	13.8	76.7	1017	4	US-09-252-991A-11322	Sequence 11322, A
38	13.8	76.7	1020	4	US-09-252-991A-9145	Sequence 9145, Ap
39	13.8	76.7	1119	4	US-09-252-991A-11028	Sequence 11028, A
40	13.8	76.7	1146	4	US-09-252-991A-9710	Sequence 9710, Ap
41	13.8	76.7	1188	4	US-09-252-991A-8025	Sequence 8025, Ap
42	13.8	76.7	1242	4	US-09-252-991A-7949	Sequence 7949, Ap
43	13.8	76.7	1255	4	US-09-659-845A-104	Sequence 104, App
44	13.8	76.7	1287	4	US-09-252-991A-8820	Sequence 8820, Ap
45	13.8	76.7	1293	4	US-09-252-991A-15351	Sequence 15351, A

ALIGNMENTS

RESULT 1

US-09-248-571-2
Sequence 2, Application US/09248571
Patent No. 6136539
GENERAL INFORMATION:
APPLICANT: BASBAUM, CAROL
APPLICANT: GALLUP, MARIANNE
APPLICANT: DAIZONG, LI
APPLICANT: GEBREMICHAEL, ASSEFA
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITION OF MUC-5 MUCIN
FILE REFERENCE: UCSF12/02
CURRENT APPLICATION NUMBER: US/09/248,571
CURRENT FILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: 60/074,398
EARLIER FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 3358
TYPE: DNA
ORGANISM: Homo sapiens
US-09-248-571-2

Query Match 82.2%; Score 14.8; DB 3; Length 3358;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCGCCGATGCAGGGGG 18
DB 999 TGCACCATGCAGGGGG 1016

RESULT 2

US-09-553-736-2
Sequence 2, Application US/09553736
Patent No. 6440672
GENERAL INFORMATION:
APPLICANT: BASBAUM, Carol
APPLICANT: GALLUP, Marianne
APPLICANT: DAIZONG, Li
APPLICANT: GEBREMICHAEL, Assefa
TITLE OF INVENTION: MUCIN GENE EXPRESSION
FILE REFERENCE: UCSF-012/03US
CURRENT APPLICATION NUMBER: US/09/553,736
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 09/248,571


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; NAME/KEY: exon 6
; LOCATION: 7745..8955
US-09-077-354B-3

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Best Local Similarity 88.9%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGGCCGCGATGCAGGGGG 18
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RESULT 5
US-09-144-085-3
; Sequence 3, Application US/09144085
; Patent No. 6280999
; GENERAL INFORMATION:
; APPLICANT: Gustafsson, Claes
; APPLICANT: Betlach, Mary C.
; APPLICANT: Ashley, Gary
; APPLICANT: Julien, Bryan
; APPLICANT: Ziermann, Rainer
; TITLE OF INVENTION: SORANGIUM POLYKETIDE SYNTHASES AND ENCODING DNA
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 30062-20020.20
; CURRENT APPLICATION NUMBER: US/09/144,085
; CURRENT FILING DATE: 1998-08-31
; EARLIER APPLICATION NUMBER: 09/010,809
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 33529
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-144-085-3

Query Match      82.2%; Score 14.8; DB 3; Length 33529;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGGCCGCGATGCAGGGGG 18
Db 30209 TGGCCAGATGCAGCGGG 30226

RESULT 6
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
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US-09-103-840A-2

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Best Local Similarity 88.9%; Pred. No. 97;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGGCCGCGATGCAGGGGG 18
Db 173979 TGGCCGATGCAGCGCG 173962

RESULT 7
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      82.2%; Score 14.8; DB 3; Length 4411529;
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGGCCGCGATGCAGGGGG 18
Db 173810 TGGCCGATGCAGCGCG 173793

RESULT 8
US-09-252-991A-4236/c
; Sequence 4236, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4236
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4236

Query Match      80.0%; Score 14.4; DB 4; Length 648;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCGCGATGCAGGGG 16
Db 263 TGGCCGAGCGCAGGGG 248
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RESULT 9
US-09-175-014-1
; Sequence 1, Application US/09175014
; Patent No. 6261802
; GENERAL INFORMATION:
; APPLICANT: Huang, Jianzhong
; APPLICANT: Jiang, Xinhe
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: ups (ugc)
; FILE REFERENCE: GM10171
; CURRENT APPLICATION NUMBER: US/09/175,014
; CURRENT FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(753)
US-09-175-014-1

Query Match 80.0%; Score 14.4; DB 3; Length 756;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCGCGATGCGAGGG 16
|||||
Db 148 TGGCGCGAGCGAGGG 163

RESULT 10
US-09-252-991A-4440
; Sequence 4440, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4440
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4440

Query Match 80.0%; Score 14.4; DB 4; Length 771;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCGCGATGCGAGGG 16
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Db 163 TGGCGCGAGCGAGGG 178

RESULT 11
US-09-328-475C-59/c
; Sequence 59, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.

; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; NAME/KEY: misc feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-59

Query Match 80.0%; Score 14.4; DB 4; Length 1024;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGGCGCGATGCGAGGGG 18
|||||
Db 805 TGGCGCGNTACAGGGGG 788

RESULT 12
US-09-252-991A-4168/c
; Sequence 4168, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4168
; LENGTH: 1488
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4168

Query Match 80.0%; Score 14.4; DB 4; Length 1488;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCGCGATGCGAGGG 16
|||||
Db 600 TGGCGCGAGCGAGGG 585

RESULT 13
US-09-252-991A-4643
; Sequence 4643, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4643
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4643
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```
Query Match      80.0%; Score 14.4; DB 4; Length 1503;
Best Local Similarity 93.8%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 TGCCTCGATGCAGGGG 16
          |||||
Db      86 TGCCTCGATGCAGGGG 101
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RESULT 14

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US-09-799-875-16
; Sequence 16, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 2870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (114)...(2000)
US-09-799-875-16
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Query Match      80.0%; Score 14.4; DB 4; Length 2870;
Best Local Similarity 93.8%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
Qy      3 CGCCGATGCAGGGGG 18
          |||||
Db     109 CGCCGATGCAGGGGG 124
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RESULT 15

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US-09-578-441-1
; Sequence 1, Application US/09578441
; Patent No. 6562571
; GENERAL INFORMATION:
; APPLICANT: Wu, J.H. David
; APPLICANT: Omata, Takeshi
; APPLICANT: Mantalaris, Athanassios
; APPLICANT: Chen, Yi-Guang
; APPLICANT: Tsai, Ying-Chueh
; TITLE OF INVENTION: HUMAN HEME-REGULATED INITIATION FACTOR 2.ALPHA KINASE
; FILE REFERENCE: 176/60571
; CURRENT APPLICATION NUMBER: US/09/578,441
; CURRENT FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/135,713
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 5
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2891
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-578-441-1
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Query Match      80.0%; Score 14.4; DB 4; Length 2891;
Best Local Similarity 93.8%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      3 CGCCGATGCAGGGGG 18
          |||||
Db     77 CGCCGATGCAGGGGG 92
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Search completed: July 2, 2004, 13:37:52
Job time : 39.2073 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:11:05 ; Search time 138.732 Seconds
(without alignments)
625.926 Million cell updates/sec

Title: US-10-068-160-18

Perfect score: 18

Sequence: 1 tgcgcgatgcaggggg 18

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	15	US-10-068-160-18
2	18	100.0	20	17	US-10-068-022-16
3	17	94.4	19	15	US-10-194-035-76
4	16.4	91.1	18	15	US-10-068-160-16
5	16.4	91.1	20	13	US-09-874-991C-499
6	16.4	91.1	20	13	US-09-874-991C-510
7	16.4	91.1	20	13	US-09-874-991C-543
8	16.4	91.1	20	15	US-10-068-160-7
9	16.4	91.1	20	15	US-10-068-160-37
10	16.4	91.1	20	15	US-10-194-035-40
11	16.4	91.1	20	15	US-10-194-035-81
12	16.4	91.1	20	15	US-10-194-035-82
13	16.4	91.1	20	15	US-10-194-035-101
14	16.4	91.1	20	17	US-10-666-022-4

15	16.4	91.1	20	17	US-10-666-022-16	Sequence 16, Appl
16	16.4	91.1	28	13	US-09-874-991C-520	Sequence 520, App
17	16.4	91.1	28	13	US-09-874-991C-532	Sequence 532, App
18	15.4	85.6	19	15	US-10-194-035-22	Sequence 22, App
19	15.4	85.6	19	15	US-10-194-035-83	Sequence 83, App
20	15.4	85.6	675	15	US-10-257-826A-239	Sequence 239, App
21	15.4	85.6	1668	17	US-10-437-963-47855	Sequence 47855, A
22	15	83.3	2712	13	US-10-282-122A-14655	Sequence 14655, A
23	14.8	82.2	18	13	US-09-874-991C-503	Sequence 503, App
24	14.8	82.2	18	13	US-09-874-991C-513	Sequence 513, App
25	14.8	82.2	18	13	US-09-874-991C-551	Sequence 551, App
26	14.8	82.2	18	15	US-10-068-160-12	Sequence 12, App
27	14.8	82.2	18	15	US-10-068-160-13	Sequence 13, App
28	14.8	82.2	18	15	US-10-068-160-14	Sequence 14, App
29	14.8	82.2	18	15	US-10-068-160-17	Sequence 17, App
30	14.8	82.2	18	15	US-10-068-160-20	Sequence 20, App
31	14.8	82.2	20	13	US-09-874-991C-494	Sequence 494, App
32	14.8	82.2	20	13	US-09-874-991C-496	Sequence 496, App
33	14.8	82.2	20	13	US-09-874-991C-497	Sequence 497, App
34	14.8	82.2	20	13	US-09-874-991C-502	Sequence 502, App
35	14.8	82.2	20	13	US-09-874-991C-504	Sequence 504, App
36	14.8	82.2	20	13	US-09-874-991C-505	Sequence 505, App
37	14.8	82.2	20	13	US-09-874-991C-507	Sequence 507, App
38	14.8	82.2	20	13	US-09-874-991C-508	Sequence 508, App
39	14.8	82.2	20	13	US-09-874-991C-512	Sequence 512, App
40	14.8	82.2	20	13	US-09-874-991C-514	Sequence 514, App
41	14.8	82.2	20	13	US-09-874-991C-538	Sequence 538, App
42	14.8	82.2	20	13	US-09-874-991C-540	Sequence 540, App
43	14.8	82.2	20	13	US-09-874-991C-541	Sequence 541, App
44	14.8	82.2	20	13	US-09-874-991C-546	Sequence 546, App
45	14.8	82.2	20	13	US-09-874-991C-550	Sequence 550, App

ALIGNMENTS

RESULT 1
US-10-068-160-18
; Sequence 18, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:

; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERHELIX, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide

US-10-068-160-18
Query Match 100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCCGATGCAGGGGG 18
Db 1 TCGCCGATGCAGGGGG 18

RESULT 2
US-10-666-022-6

Sequence 6, Application US/10666022
Publication No. US20040105872A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the
Secretary of the Department of Health and Human Services
APPLICANT: Klinman, Dennis M.
APPLICANT: Verthelyi, Daniela
TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
SUBJECTS WITH IMMUNOSTIMULATORY CPG
FILE REFERENCE: 4239-66899
CURRENT APPLICATION NUMBER: US/10/666,022
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,944
PRIOR FILING DATE: 2002-09-18
NUMBER OF SEQ ID NOS: 191
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic
NAME/KEY: misc feature
LOCATION: (1)..(20)
OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-6

Query Match 100.0%; Score 18; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGCCCGATCGAGGGGG 18
DB 3 TGGCCCGATCGAGGGGG 20

RESULT 3
US-10-194-035-76
Sequence 76, Application US/10194035
Publication No. US20030144229A1
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, DENNIS
APPLICANT: ISHII, Ken
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-63317
CURRENT APPLICATION NUMBER: US/10/194,035
CURRENT FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: PCT/US01/01122
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/176,115
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 119
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 76
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-76

Query Match 94.4%; Score 17; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGCCCGATCGAGGGGG 17
DB 3 TGGCCCGATCGAGGGGG 19

RESULT 4
US-10-068-160-16
Sequence 16, Application US/10068160
Publication No. US2003006040A1
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, DENNIS
APPLICANT: ISHII, Ken
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-61999
CURRENT APPLICATION NUMBER: US/10/068,160
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/128,898
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-10-068-160-16

Query Match 91.1%; Score 15.4; DB 15; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATCGAGGGGG 18
DB 1 TGGCCCGATCGAGGGGG 18

RESULT 5
US-09-874-991C-499
Sequence 499, Application US/09874991C
Publication No. US20040052763A1
GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: KLINMAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787,0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 499
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-499

Query Match 91.1%; Score 15.4; DB 13; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATCGAGGGGG 18
DB 3 TGGCCCGATCGAGGGGG 20

RESULT 6
US-09-874-991C-510
Sequence 510, Application US/09874991C
Publication No. US20040052763A1

GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: KLINMAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
CURRENT APPLICATION NUMBER: US/09/874.991C
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 510
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-510

Query Match 91.1%; Score 16.4; DB 13; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCGAGGGGG 18
DB 3 TGCACCGATGCGAGGGGG 20

RESULT 7
US-09-874-991C-543
Sequence 543, Application US/09874991C
Publication No. US20040052763A1
GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: KLINMAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
CURRENT APPLICATION NUMBER: US/09/874.991C
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 543
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-543

Query Match 91.1%; Score 16.4; DB 13; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCGAGGGGG 18
DB 3 TGCACCGATGCGAGGGGG 20

RESULT 8
US-10-068-160-7
Sequence 7, Application US/10068160
Publication No. US2003006040A1
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, DENNIS
APPLICANT: ISHII, KEN
APPLICANT: VERTHELYI, Daniela
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE

FILE REFERENCE: 4239-61999
CURRENT APPLICATION NUMBER: US/10/068,160
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/128,898
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patent in version 3.1
SEQ ID NO 7
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-10-068-160-7

Query Match 91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCGAGGGGG 18
DB 3 TGCCTCGATGCGAGGGGG 20

RESULT 9
US-10-068-160-37
Sequence 37, Application US/10068160
Publication No. US20030060440A1
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, DENNIS
APPLICANT: ISHII, KEN
APPLICANT: VERTHELYI, Daniela
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-61999
CURRENT APPLICATION NUMBER: US/10/068,160
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/128,898
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patent in version 3.1
SEQ ID NO 37
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-10-068-160-37

Query Match 91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCGAGGGGG 18
DB 3 TGCACCGATGCGAGGGGG 20

RESULT 10
US-10-194-035-40
Sequence 40, Application US/10194035
Publication No. US20030144229A1
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, DENNIS
APPLICANT: ISHII, KEN
APPLICANT: VERTHELYI, Daniela
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-63317
CURRENT APPLICATION NUMBER: US/10/194,035
CURRENT FILING DATE: 2002-07-12

; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-40

Query Match 91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCAGGGGGG 18
||| ||||| ||||| |||||
Db 3 TGGCTCGATGCAGGGGGG 20

RESULT 11
US-10-194-035-81
; Sequence 81, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 81
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-81

Query Match 91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCAGGGGGG 18
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RESULT 12
US-10-194-035-82
; Sequence 82, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035

; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-82

Query Match 91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCAGGGGGG 18
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Db 3 TGGCTCGATGCAGGGGGG 20

RESULT 13
US-10-194-035-101
; Sequence 101, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 101
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-101

Query Match 91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCAGGGGGG 18
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Db 3 TGGCTCGATGCAGGGGGG 20

RESULT 14
US-10-666-022-4
; Sequence 4, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Verthelyi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMIS
; TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG
; FILE REFERENCE: 4239-66899

; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-4

Query Match 91.1%; Score 16.4; DB 17; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGCCGATGCAGGGGG 18
Db 3 TGGTCGATGCAGGGGG 20

RESULT 15
US-10-666-022-16
; Sequence 16, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Verhelmi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-666-022-16

Query Match 91.1%; Score 16.4; DB 17; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGCCGATGCAGGGGG 18
Db 3 TGGTCGATGCAGGGGG 20

Search completed: July 2, 2004, 13:58:26
Job time : 139.732 secs

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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:36:05 ; Search time 704.146 Seconds
(without alignments)
1231.080 Million cell updates/sec

Title: US-10-068-160-1

Perfect score: 20

Sequence: 1 ggtgcatcgatgcaggggg 20

Scoring table:

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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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39: em.htgo.hum.*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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2	20	100.0	20	6	AX194434	Sequence
3	20	100.0	20	6	AX194437	Sequence
4	20	100.0	20	6	AX194438	Sequence
5	20	100.0	20	6	AX194443	Sequence
6	20	100.0	20	6	AX194472	Sequence
7	20	100.0	20	6	AX352198	Sequence
8	20	100.0	20	6	AX352209	Sequence
9	20	100.0	20	6	AX352242	Sequence
10	20	100.0	20	6	AX465382	Sequence
11	20	100.0	20	6	AX465384	Sequence
12	20	100.0	20	6	AX465387	Sequence
13	20	100.0	20	6	AX465388	Sequence
14	20	100.0	20	6	AX465393	Sequence
15	20	100.0	20	6	AX465422	Sequence
16	20	100.0	20	6	AX816067	Sequence
17	20	100.0	20	6	AX352204	Sequence
18	20	100.0	20	6	AX352248	Sequence
19	20	100.0	28	6	AX352219	Sequence
20	20	100.0	28	6	AX352231	Sequence
21	20	100.0	29	6	AX352237	Sequence
22	20	100.0	30	6	AX352225	Sequence
23	20	100.0	30	6	AX352230	Sequence
24	20	100.0	32	6	AX352167	Sequence
25	19	95.0	19	6	AX194453	Sequence
26	19	95.0	19	6	AX194473	Sequence
27	19	95.0	19	6	AX465403	Sequence
28	19	95.0	19	6	AX465423	Sequence
29	18.4	92.0	20	6	AX194440	Sequence
30	18.4	92.0	20	6	AX194481	Sequence
31	18.4	92.0	20	6	AX194482	Sequence
32	18.4	92.0	20	6	AX194500	Sequence
33	18.4	92.0	20	6	AX194501	Sequence
34	18.4	92.0	20	6	AX194504	Sequence
35	18.4	92.0	20	6	AX194506	Sequence
36	18.4	92.0	20	6	AX194507	Sequence
37	18.4	92.0	20	6	AX352202	Sequence
38	18.4	92.0	20	6	AX352203	Sequence
39	18.4	92.0	20	6	AX352213	Sequence
40	18.4	92.0	20	6	AX352214	Sequence
41	18.4	92.0	20	6	AX352246	Sequence
42	18.4	92.0	20	6	AX352247	Sequence
43	18.4	92.0	20	6	AX465390	Sequence
44	18.4	92.0	20	6	AX465431	Sequence
45	18.4	92.0	20	6	AX465432	Sequence

ALIGNMENTS

RESULT 1
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LOCUS AX194432
DEFINITION Sequence 32 from Patent WO0151500.
ACCESSION AX194432
VERSION AX194432.1 GI:15385088
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Klimman,D., Ishii,K. and Verthelyi,D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 32 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)

20 bp DNA linear PAT 28-AUG-2001


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ORIGIN

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  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 2
AX194434
LOCUS AX194434 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 34 from Patent WO0151500.
ACCESSION AX194434
VERSION AX194434.1 GI:15385090
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
  1
  Klinman,D., Ishii,K. and Verthelyi,D.
  Oligodeoxynucleotide and its use to induce an immune response
  Patent: WO 0151500-A 34 19-JUL-2001;
  JOURNAL Secretary of the Department of Health and Human Services (US)
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  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGAGGGGG 20
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Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 3
AX194437
LOCUS AX194437 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 37 from Patent WO0151500.
ACCESSION AX194437
VERSION AX194437.1 GI:15385093
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
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REFERENCE
  1
  Klinman,D., Ishii,K. and Verthelyi,D.
  Oligodeoxynucleotide and its use to induce an immune response
  Patent: WO 0151500-A 37 19-JUL-2001;
  JOURNAL Secretary of the Department of Health and Human Services (US)
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  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
AX194438
LOCUS AX194438 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 38 from Patent WO0151500.
ACCESSION AX194438
VERSION AX194438.1 GI:15385094
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
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  Klinman,D., Ishii,K. and Verthelyi,D.
  Oligodeoxynucleotide and its use to induce an immune response
  Patent: WO 0151500-A 38 19-JUL-2001;
  JOURNAL Secretary of the Department of Health and Human Services (US)
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RESULT 5
AX194443
LOCUS AX194443 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 43 from Patent WO0151500.
ACCESSION AX194443
VERSION AX194443.1 GI:15385099
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
  1
  Klinman,D., Ishii,K. and Verthelyi,D.
  Oligodeoxynucleotide and its use to induce an immune response
  Patent: WO 0151500-A 43 19-JUL-2001;
  JOURNAL Secretary of the Department of Health and Human Services (US)
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ORIGIN

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RESULT 6
AX194443
LOCUS AX194443 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 43 from Patent WO0151500.
ACCESSION AX194443
VERSION AX194443.1 GI:15385099
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
  1
  Klinman,D., Ishii,K. and Verthelyi,D.
  Oligodeoxynucleotide and its use to induce an immune response
  Patent: WO 0151500-A 43 19-JUL-2001;
  JOURNAL Secretary of the Department of Health and Human Services (US)
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ORIGIN

Query Match
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  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGTGCATCGATCGAGGGGG 20

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AX194472
LOCUS AX194472 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 72 from Patent WO0151500.
ACCESSION AX194472
VERSION AX194472.1 GI:15385128
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 72 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
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Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGTGCATCGATGCAGGGGG 20
RESULT 7
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LOCUS AX352198 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 494 from Patent WO0193902.
ACCESSION AX352198
VERSION AX352198.1 GI:18617481
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Mond,J.J., Flora,M. and Klimman,D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 494 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:32630"
/note="Synthetic HDR"
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Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGTGCATCGATGCAGGGGG 20
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Db 1 GGTGCATCGATGCAGGGGG 20
RESULT 8
AX352209
LOCUS AX352209 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 505 from Patent WO0193902.
ACCESSION AX352209
VERSION AX352209.1 GI:18617492
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
AUTHORS Mond,J.J., Flora,M. and Klimman,D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 505 13-DEC-2001;
Biosynexus Incorporated (US)
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source Location/Qualifiers
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Synthetic HDR"
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Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGTGCATCGATGCAGGGGG 20
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Db 1 GGTGCATCGATGCAGGGGG 20
RESULT 9
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LOCUS AX352242 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 538 from Patent WO0193902.
ACCESSION AX352242
VERSION AX352242.1 GI:18617525
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Mond,J.J., Flora,M. and Klimman,D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 538 13-DEC-2001;
Biosynexus Incorporated (US)
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source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 16;
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Db 1 GGTGCATCGATGCAGGGGG 20
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LOCUS AX465382 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 50 from Patent WO0211761.
ACCESSION AX465382
VERSION AX465382.1 GI:21899745
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Mond,J.J., Prince,G. and Klimman,D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 50 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES
source Location/Qualifiers
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ORIGIN

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GGTGTCATCGATCGAGGGGG 20
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LOCUS AX465384 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 52 from Patent WO0211761.
ACCESSION AX465384
VERSION AX465384.1 GI:21899747

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mond, J.J., Prince, G. and Klinman, D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 52 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)

FEATURES

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DB 1 GGTGTCATCGATCGAGGGGG 20
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RESULT 12

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LOCUS AX465387 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 55 from Patent WO0211761.
ACCESSION AX465387
VERSION AX465387.1 GI:21899750

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mond, J.J., Prince, G. and Klinman, D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 55 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)

FEATURES

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GGTGTCATCGATCGAGGGGG 20
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RESULT 13

AX465388
LOCUS AX465388 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 56 from Patent WO0211761.
ACCESSION AX465388
VERSION AX465388.1 GI:21899751

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mond, J.J., Prince, G. and Klinman, D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 56 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)

FEATURES

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Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTCATCGATCGAGGGGG 20
|||||
DB 1 GGTGTCATCGATCGAGGGGG 20
|||||

RESULT 14

AX465393
LOCUS AX465393 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 61 from Patent WO0211761.
ACCESSION AX465393
VERSION AX465393.1 GI:21899756

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mond, J.J., Prince, G. and Klinman, D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 61 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)

FEATURES

source
1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTCATCGATCGAGGGGG 20
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DB 1 GGTGTCATCGATCGAGGGGG 20
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RESULT 15
AX465422
LOCUS      AX465422          20 bp      DNA      linear      PAT 16-JUL-2002
DEFINITION Sequence 90 from Patent WO0211761.
ACCESSION  AX465422
VERSION    AX465422.1  GI:21899785
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS   Mond, J.J., Prince, G. and Klinman, D.M.
TITLE     Vaccine against RSV.
JOURNAL   Patent: WO 0211761-A 90 14-FEB-2002;
           HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
           MEDICINE (US)
FEATURES   Location/Qualifiers
           1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic oligonucleotide"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GGTGCATCGATCGAGGGGG 20
Db      1  GGTGCATCGATCGAGGGGG 20
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|||||

Search completed: July 2, 2004, 10:07:54
Job time : 705.146 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 06:05:50 ; Search time 149.878 Seconds
(without alignments)
566.887 Million cell updates/sec

Title: US-10-068-160-1

Perfect score: 20

Sequence: 1 ggtgcatgagcagggggg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002s:*
- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	4 AAC80652	Aac80652 Immunogen
2	20	100.0	20	4 AAC80614	Aac80614 Immunogen
3	20	100.0	20	4 AAC80612	Aac80612 Immunogen
4	20	100.0	20	4 AAC80617	Aac80617 Immunogen
5	20	100.0	20	4 AAC80618	Aac80618 Immunogen
6	20	100.0	20	4 AAC80623	Aac80623 Immunogen
7	20	100.0	20	4 AAC80622	Aac80622 Immunogen
8	20	100.0	20	4 AAS09582	Aas09582 Immunore
9	20	100.0	20	4 AAS09587	Aas09587 Immunore
10	20	100.0	20	4 AAS09593	Aas09593 Immunore
11	20	100.0	20	4 AAS09584	Aas09584 Immunore
12	20	100.0	20	4 AAS09588	Aas09588 Immunore
13	20	100.0	20	6 ABL35568	Ab135568 Immunosti
14	20	100.0	20	6 ABL35579	Ab135579 Immunosti
15	20	100.0	20	6 ABL35612	Ab135612 Immunosti
16	20	100.0	20	6 ABK46500	Abk46500 Immunosti
17	20	100.0	20	6 ABK46460	Abk46460 Immunosti
18	20	100.0	20	6 ABK46465	Abk46465 Immunosti
19	20	100.0	20	6 ABK46471	Abk46471 Immunosti
20	20	100.0	20	6 ABK46462	Abk46462 Immunosti
21	20	100.0	20	6 ABK46466	Abk46466 Immunosti
22	20	100.0	20	6 ACC48309	Acc48309 CpG oligo
23	20	100.0	20	7 ACC48295	Acc48295 CpG oligo

24	20	100.0	20	7 ACC48310	Acc48310 CpG oligo
25	20	100.0	20	7 ACC48316	Acc48316 CpG oligo
26	20	100.0	20	8 ACC83150	Acc83150 D class O
27	20	100.0	20	8 ACC83115	Acc83115 D class C
28	20	100.0	20	8 ACC83151	Acc83151 D class O
29	20	100.0	20	8 ACC83114	Acc83114 D class C
30	20	100.0	20	8 ACC83121	Acc83121 D class C
31	20	100.0	20	9 ADB84186	Adb84186 CpG conta
32	20	100.0	20	9 ADC51789	Adc51789 D19 SEQ I
33	20	100.0	20	9 ADD01074	Add01074 CpG D oli
34	20	100.0	20	9 ADD01048	Add01048 CpG D oli
35	20	100.0	22	6 ABL35574	Ab135574 Immunosti
36	20	100.0	22	6 ABL35618	Ab135618 Immunosti
37	20	100.0	28	6 ABL35601	Ab135601 Immunosti
38	20	100.0	28	6 ABL35589	Ab135589 Immunosti
39	20	100.0	29	6 ABL35607	Ab135607 Immunosti
40	20	100.0	30	6 ABL35600	Ab135600 Immunosti
41	20	100.0	30	6 ABL35595	Ab135595 Immunosti
42	20	100.0	32	6 ABL35537	Ab135537 Immunosti
43	20	100.0	32	7 ACC48325	Acc48325 CpG oligo
44	20	100.0	32	7 ACC48323	Acc48323 CpG oligo
45	20	100.0	32	7 ACC48324	Acc48324 CpG oligo

ALIGNMENTS

RESULT 1

AAC80652

ID AAC80652 standard; DNA; 20 BP.

XX AC AAC80652;

XX DT 14-FEB-2001 (first entry)

XX DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:72.

XX KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
cell-mediated immune response; T-cell response; humoral response;
B-cell response; antibody production; immune response induction; vaccine;
allergy; asthma; infection; bacterial; viral; fungal; protozoal;
parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
immune deficiency; biological warfare agent; cytostatic; antiarthritic;
antimicrobial; antiallergic; protozoacide; tuberculostatic;
antiasthmatic; dermatological; phosphorothioate; ss.
XX KW Synthetic.

XX OS WO200061151-A2.

XX PN 19-OCT-2000.

XX PD 12-APR-2000; 2000WO-US009839.

XX PF 12-APR-1999; 99US-0128898P.

XX PR (KLIN/) KLINMAN D.

XX PA (ISHI/) ISHII K.

XX PA (VERT/) VERTHELYI D.

XX PI Klinman D, Ishii K, Verthelyi D;

XX PI WPI; 2001-006880/01.

XX DR Novel oligonucleotides useful for the prevention and treatment of

XX PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms

XX PT resulting from exposure to a bio-warfare agent.

XX PS Claim 4; Page 35; 46pp; English.

XX CC The invention relates to novel immunogenic CpG oligodeoxynucleotides

(AAC80581-C80723). The oligonucleotide are at least 10 bases long and comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RV-CpG-RY-3'. The central CpG motif is unmethylated, and the oligonucleotides optionally have phosphorothioate linkages which make them more resistant to degradation. The invention also relates to an oligonucleotide delivery complex comprising an oligonucleotide of the invention and a targeting agent, and a pharmaceutical composition comprising the oligonucleotide delivery complex. The oligonucleotides are able to induce either a cell-mediated (T-cell) response or a humoral (B-cell, antibody) response, with oligonucleotides of the sequence 5'-RV-CpG-RY-3' being able to induce a cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3' being able to induce a humoral response. It is thought that after administration, the oligonucleotide acts on antigen-presenting cells (e.g., macrophages and dendritic cells), which then release cytokines, leading to activation of natural killer (NK) cells. A cell-mediated or humoral response can then occur by activation of T- or B-cells. The induction of an immune response is useful for treating, preventing or ameliorating an allergic reaction (preferably asthma), or an infection, where an immunogenic CpG oligonucleotide is administered either alone or in combination with an anti-allergenic agent or anti-infectious agent. The allergic conditions which may be treated include eczema, allergic rhinitis, hayfever, urticaria, food allergies and other atopic conditions, and the infections which may be treated include viral, bacterial, fungal and protozoal infections such as tuberculosis, AIDS, leishmania and schistosomiasis. Immune response induction may also be used in the treatment of an autoimmune disorder (e.g., lupus erythematosus, rheumatoid arthritis and multiple sclerosis), a disease associated with immune system deficiency, and symptoms resulting from exposure to an agent of biological warfare. An immunogenic CpG oligonucleotide, either alone or in combination with an anti-cancer agent, is useful for treating solid tumour cancer. The induction of an immune response is used in antisense therapy and to improve the efficacy of a vaccine. The oligonucleotide is preferably administered to lymphocytes ex vivo, producing activated lymphocytes which are then administered to the host. The present sequence represents an immunogenic CpG oligodeoxynucleotide of the invention

Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCATCGATGCAGGGGGG 20
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 Db 1 GGTCATCGATGCAGGGGGG 20

RESULT 2
 AAC80614
 ID AAC80614 standard; DNA; 20 BP.
 AC AAC80614;
 XX
 DT 14-FEB-2001 (first entry)
 XX
 DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:34.
 XX
 KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
 immunogenic; cytokine release; natural killer cell; NK cell activation;
 cell-mediated immune response; T-cell response; humoral response; vaccine;
 B-cell response; antibody production; immune response induction; allergic
 allergy; asthma; infection; bacterial; viral; fungal; protozoal;
 parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
 rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
 immune deficiency; biological warfare agent; cytostatic; antiarthritic;
 antimicrobial; antiallergic; protozoic; tuberculostatic;
 antiasthmatic; dermatological; phosphorothioate; ss.

OS Synthetic.
 XX
 XX WO200061151-A2.
 XX

PD 19-OCT-2000.
 XX
 PF 12-APR-2000; 2000WO-US009839.
 XX
 PR 12-APR-1999; 99US-0128898P.
 XX
 PA (KLIN/) KLINMAN D.
 PA (ISHI/) ISHII K.
 PA (VERT/) VERTHELYI D.
 XX
 PI Kliman D, Ishii K, Verthelyi D;
 XX
 WIPI; 2001-006880/01.
 DR
 XX Novel oligonucleotides useful for the prevention and treatment of
 allergies, cancer, and autoimmune disorders and for ameliorating symptoms
 resulting from exposure to a bio-warfare agent.
 PT
 PT
 PT
 PT
 PT
 PS Claim 4; Page 29; 45pp; English.
 XX
 XX The invention relates to novel immunogenic CpG oligodeoxynucleotides
 (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
 comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RV-CpG-RY-
 3'. The central CpG motif is unmethylated, and the oligonucleotides
 optionally have phosphorothioate linkages which make them more resistant
 to degradation. The invention also relates to an oligonucleotide delivery
 complex comprising an oligonucleotide of the invention and a targeting
 agent, and a pharmaceutical composition comprising the oligonucleotide
 delivery complex. The oligonucleotides are able to induce either a cell-
 mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 oligonucleotides of the sequence 5'-RV-CpG-RY-3' being able to induce a
 cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
 being able to induce a humoral response. It is thought that after
 administration, the oligonucleotide acts on antigen-presenting cells
 (e.g., macrophages and dendritic cells), which then release cytokines,
 leading to activation of natural killer (NK) cells. A cell-mediated or
 humoral response can then occur by activation of T- or B-cells. The
 induction of an immune response is useful for treating, preventing or
 ameliorating an allergic reaction (preferably asthma), or an infection,
 where an immunogenic CpG oligonucleotide is administered either alone or
 in combination with an anti-allergenic agent or anti-infectious agent.
 The allergic conditions which may be treated include eczema, allergic
 rhinitis, hayfever, urticaria, food allergies and other atopic
 conditions, and the infections which may be treated include viral,
 bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 leishmania and schistosomiasis. Immune response induction may also be
 used in the treatment of an autoimmune disorder (e.g., lupus
 erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 associated with immune system deficiency, and symptoms resulting from
 exposure to an agent of biological warfare. An immunogenic CpG
 oligonucleotide, either alone or in combination with an anti-cancer
 agent, is useful for treating solid tumour cancer. The induction of an
 immune response is used in antisense therapy and to improve the efficacy
 of a vaccine. The oligonucleotide is preferably administered to
 lymphocytes ex vivo, producing activated lymphocytes which are then
 administered to the host. The present sequence represents an immunogenic
 CpG oligodeoxynucleotide of the invention

Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCATCGATGCAGGGGGG 20
 |||||
 Db 1 GGTCATCGATGCAGGGGGG 20

RESULT 3
 AAC80612
 ID AAC80612 standard; DNA; 20 BP.
 XX

CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g., macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergenic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic
 CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antisense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention
 XX
 SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTGCATCGATGCAGGGGG 20
 DB 1 GGTGCATCGATGCAGGGGG 20
 RESULT 5
 AAC80618
 ID AAC80618 standard; DNA; 20 BP.
 XX
 AC AAC80618;
 XX
 DT 14-FEB-2001 (first entry)
 XX
 DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:38.
 XX
 KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
 KW immunogenic; cytokine release; natural killer cell; NK cell activation;
 KW cell-mediated immune response; T-cell response; humoral response;
 KW B-cell response; antibody production; immune response induction; vaccine;
 KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
 KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
 KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
 KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
 KW antimicrobial; antiallergic; protozoicide; tuberculostatic;
 KW antiasthmatic; dermatological; phosphorothioate; ss.
 OS Synthetic.
 XX
 XX
 PN WO200061151-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 12-APR-2000; 2000WO-US0009839.
 XX
 PR 12-APR-1999; 99US-0128898P.
 XX
 PA (KLIN/) KLINMAN D.
 PA (ISHI/) ISHII K.
 PA (VERT/) VERTHELYI D.
 XX

PI Klinman D, Ishii K, Verthelyi D;
 WPI: 2001-006880/01.
 Novel oligonucleotides useful for the prevention and treatment of
 allergies, cancer, and autoimmune disorders and for ameliorating symptoms
 resulting from exposure to a bio-warfare agent.
 Claim 4; Page 30; 46pp; English.
 The invention relates to novel immunogenic CpG oligodeoxynucleotides
 (AAC8061-C80723). The oligonucleotide are at least 10 bases long and
 comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 -3'. The central CpG motif is unmethylated, and the oligonucleotides
 optionally have phosphorothioate linkages which make them more resistant
 to degradation. The invention also relates to an oligonucleotide delivery
 complex comprising an oligonucleotide of the invention and a targeting
 agent, and a pharmaceutical composition comprising the oligonucleotide
 mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
 cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
 being able to induce a humoral response. It is thought that after
 administration, the oligonucleotide acts on antigen-presenting cells
 (e.g., macrophages and dendritic cells), which then release cytokines,
 leading to activation of natural killer (NK) cells. A cell-mediated or
 humoral response can then occur by activation of T- or B-cells. The
 induction of an immune response is useful for treating, preventing or
 ameliorating an allergic reaction (preferably asthma), or an infection,
 where an immunogenic CpG oligonucleotide is administered either alone or
 in combination with an anti-allergenic agent or anti-infectious agent.
 The allergic conditions which may be treated include eczema, allergic
 rhinitis, hayfever, urticaria, food allergies and other atopic
 conditions, and the infections which may be treated include viral,
 bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 leishmania and schistosomiasis. Immune response induction may also be
 used in the treatment of an autoimmune disorder (e.g., lupus
 erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 associated with immune system deficiency, and symptoms resulting from
 exposure to an agent of biological warfare. An immunogenic CpG
 oligonucleotide, either alone or in combination with an anti-cancer
 agent, is useful for treating solid tumour cancer. The induction of an
 immune response is used in antisense therapy and to improve the efficacy
 of a vaccine. The oligonucleotide is preferably administered to
 lymphocytes ex vivo, producing activated lymphocytes which are then
 administered to the host. The present sequence represents an immunogenic
 CpG oligodeoxynucleotide of the invention
 XX
 SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTGCATCGATGCAGGGGG 20
 DB 1 GGTGCATCGATGCAGGGGG 20
 RESULT 6
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 ID AAC80623 standard; DNA; 20 BP.
 XX
 AC AAC80623;
 XX
 DT 14-FEB-2001 (first entry)
 XX
 DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:43.
 XX
 KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
 KW immunogenic; cytokine release; natural killer cell; NK cell activation;
 KW cell-mediated immune response; T-cell response; humoral response;
 KW B-cell response; antibody production; immune response induction; vaccine;
 XX

allergy; asthma, infection; bacterial; viral; fungal; protozoal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer; immune deficiency; biological warfare agent; cytostatic; antiarthritic; antimicrobial; antiallergic; protozoicide; tuberculostatic; antiasthmatic; dermatological; phosphorothioate; ss.

Synthetic.

WO200061151-A2.

19-OCT-2000.

12-APR-2000; 2000WO-US009839.

12-APR-1999; 99US-0128998P.

(KLIN/) KLINMAN D.

(ISHI/) ISHII K.

(VERT/) VERTHELYI D.

Klinman D, Ishii K, Verthelyi D;

WPI; 2001-006880/01.

Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent.

Claim 4; Page 30; 46pp; English.

The invention relates to novel immunogenic CpG oligodeoxynucleotides (AAC80581-C80723). The oligonucleotide are at least 10 bases long and comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY-3'. The central CpG motif is unmethylated, and the oligonucleotides optionally have phosphorothioate linkages which make them more resistant to degradation. The invention also relates to an oligonucleotide delivery complex comprising an oligonucleotide of the invention and a targeting agent, and a pharmaceutical composition comprising the oligonucleotide delivery complex. The oligonucleotides are able to induce either a cell-mediated (T-cell) response or a humoral (B-cell, antibody) response, with oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3' being able to induce a humoral response. It is thought that after administration, the oligonucleotide acts on antigen-presenting cells (e.g., macrophages and dendritic cells), which then release cytokines, leading to activation of natural killer (NK) cells. A cell-mediated or humoral response can then occur by activation of T- or B-cells. The induction of an immune response is useful for treating, preventing or ameliorating an allergic reaction (preferably asthma), or an infection, where an immunogenic CpG oligonucleotide is administered either alone or in combination with an anti-allergenic agent or anti-infectious agent. The allergic conditions which may be treated include eczema, allergic rhinitis, hayfever, urticaria, food allergies and other atopic conditions, and the infections which may be treated include viral, bacterial, fungal and protozoal infections such as tuberculosis, AIDS, leishmania and schistosomiasis. Immune response induction may also be used in the treatment of an autoimmune disorder (e.g., lupus erythematosus, rheumatoid arthritis and multiple sclerosis), a disease associated with immune system deficiency, and symptoms resulting from exposure to an agent of biological warfare. An immunogenic CpG oligonucleotide, either alone or in combination with an anti-cancer agent, is useful for treating solid tumour cancer. The induction of an immune response is used in antisense therapy and to improve the efficacy of a vaccine. The oligonucleotide is preferably administered to lymphocytes *ex vivo*, producing activated lymphocytes which are then administered to the host. The present sequence represents an immunogenic CpG oligodeoxynucleotide of the invention

Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGATCGATGCGAGGGGG 20
|||||

DB 1 GGTGATCGATGCGAGGGGG 20
|||||

RESULT 7

AAS09622

ID AAS09622 standard; DNA; 20 BP.

AC AAS09622;

XX

XX 26-SEP-2001 (first entry)

XX

XX Immunoreactive CpG sequence-containing oligonucleotide #72.

XX

XX CpG sequence; immune response; non-B cell activation; interferon gamma; IFN-gamma; humoral; antibody production; interleukin-6 production; therapeutic; allergy; asthma; cancer; autoimmune disorder; infection; bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; ss.

XX Synthetic.

OS

XX WO200151500-A1.

XX

XX 19-JUL-2001.

XX

XX 12-JAN-2001; 2001WO-US001122.

XX

XX 14-JAN-2000; 2000US-0176115P.

XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

XX Klinman D, Ishii K, Verthelyi D;

XX

XX WPI; 2001-442129/47.

XX

XX Oligodeoxynucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG sequences.

XX

XX Claim 5; Page 39; 48pp; English.

XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10 nucleotides comprising multiple CpG sequences, where one of the CpG sequences is different from another of the multiple CpG sequences. The ODN are useful for inducing an immune response, preferably a cell-mediated immune response, involving non-B cell activation, interferon gamma (IFN-gamma) production or a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma, cancer, e.g. solid tumour cancer, a disease associated with the immune system e.g. autoimmune disorder or an immune system deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antisense therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines against hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, Anthrax and Listeria

```

XX SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTCATCGATCGAGGGGG 20
Db 1 GGTGTCATCGATCGAGGGGG 20

RESULT 8
AAS09582
ID AAS09582 standard; DNA; 20 BP.
AC AAS09582;
XX
XX 26-SEP-2001 (first entry)
XX
XX Immunoreactive CpG sequence-containing oligonucleotide #32.
XX
XX CpG sequence; immune response; non-B cell activation; interferon gamma;
XX IFN-gamma; humoral; antibody production; interleukin-6 production;
XX therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
XX bio-warfare; vaccine; antitense therapy; eczema; allergic rhinitis;
XX coryza; hay fever; urticaria; hives; food allergy; atopic condition;
XX hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
XX lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
XX schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
XX Leishmania; Ebola; Anthrax; Listeria; ss.
XX Synthetic.
XX
XX WQ200151500-A1.
XX 19-JUL-2001.
XX
XX 12-JAN-2001; 2001WO-US001122.
XX
XX 14-JAN-2000; 2000US-0176115P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Klinman D, Ishii K, Verthelyi D;
XX WPI; 2001-442129/47.
XX
XX Oligodeoxynucleotides for inducing an immune response to treat and
XX prevent an allergic reaction; cancer, an autoimmune disorder and symptoms
XX resulting from exposure to bio-warfare agents, comprise multiple CpG
XX sequences.
XX
XX Claim 5; Page 32; 48pp; English.
XX
XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
XX nucleotides comprising multiple CpG sequences, where one of the CpG
XX sequences is different from another of the multiple CpG sequences. The
XX ODN are useful for inducing an immune response, preferably a cell-
XX mediated immune response, involving non-B cell activation, interferon
XX gamma (IFN-gamma) production or a humoral immune response involving B
XX cell activation, antibody and interleukin-6 production in a host, for
XX treating, preventing or ameliorating an allergic reaction, e.g. asthma,
XX cancer, e.g. solid tumour cancer, a disease associated with the immune
XX system e.g. autoimmune disorder or an immune system deficiency, infection
XX or a symptom resulting from exposure to bio-warfare agent in a human. The
XX induction of immune response improves the efficacy of a vaccine and is
XX used in antitense therapy. The ODN are useful for treating, preventing or
XX ameliorating allergic reactions, including eczema, allergic rhinitis or
XX coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
XX and other atopic conditions, for improving the efficacy of vaccines
XX against hepatitis A, B and C, human immunodeficiency virus (HIV) and
XX malaria, for treating immune system deficiencies, e.g. lupus

```

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CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTCATCGATCGAGGGGG 20
Db 1 GGTGTCATCGATCGAGGGGG 20

RESULT 9
AAS09587
ID AAS09587 standard; DNA; 20 BP.
XX
XX AAS09587;
XX
XX 26-SEP-2001 (first entry)
XX
XX Immunoreactive CpG sequence-containing oligonucleotide #37.
XX
XX CpG sequence; immune response; non-B cell activation; interferon gamma;
XX IFN-gamma; humoral; antibody production; interleukin-6 production;
XX therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
XX bio-warfare; vaccine; antitense therapy; eczema; allergic rhinitis;
XX coryza; hay fever; urticaria; hives; food allergy; atopic condition;
XX hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
XX lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
XX schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
XX Leishmania; Ebola; Anthrax; Listeria; ss.
XX Synthetic.
XX
XX WQ200151500-A1.
XX 19-JUL-2001.
XX
XX 12-JAN-2001; 2001WO-US001122.
XX
XX 14-JAN-2000; 2000US-0176115P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Klinman D, Ishii K, Verthelyi D;
XX WPI; 2001-442129/47.
XX
XX Oligodeoxynucleotides for inducing an immune response to treat and
XX prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
XX resulting from exposure to bio-warfare agents, comprise multiple CpG
XX sequences.
XX
XX Claim 5; Page 33; 48pp; English.
XX
XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
XX nucleotides comprising multiple CpG sequences, where one of the CpG
XX sequences is different from another of the multiple CpG sequences. The
XX ODN are useful for inducing an immune response, preferably a cell-
XX mediated immune response, involving non-B cell activation, interferon
XX gamma (IFN-gamma) production or a humoral immune response involving B
XX cell activation, antibody and interleukin-6 production in a host, for
XX treating, preventing or ameliorating an allergic reaction, e.g. asthma,
XX cancer, e.g. solid tumour cancer, a disease associated with the immune
XX system e.g. autoimmune disorder or an immune system deficiency, infection
XX or a symptom resulting from exposure to bio-warfare agent in a human. The
XX induction of immune response improves the efficacy of a vaccine and is
XX used in antitense therapy. The ODN are useful for treating, preventing or
XX ameliorating allergic reactions, including eczema, allergic rhinitis or
XX coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
XX and other atopic conditions, for improving the efficacy of vaccines
XX against hepatitis A, B and C, human immunodeficiency virus (HIV) and
XX malaria, for treating immune system deficiencies, e.g. lupus

```

CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematous and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria

XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTCATCGATCGAGGGGG 20
 |||||
 DB 1 GGTGTCATCGATCGAGGGGG 20

RESULT 10

AA09593
 ID AA09593 standard; DNA; 20 BP.

XX AA09593;

AC AA09593;

DT 26-SEP-2001 (first entry)

DE Immunoreactive CpG sequence-containing oligonucleotide #43.

XX CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.

XX Synthetic.

XX WO200151500-A1.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-US001122.

XX 14-JAN-2000; 2000US-0176115P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Klinman D, Ishii K, Verthelyi D;

XX WPI; 2001-442129/47.

XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.

XX Claim 5; Page 34; 48pp; English.

XX AA09551-AA09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,

CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematous and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria

XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTCATCGATCGAGGGGG 20
 |||||
 DB 1 GGTGTCATCGATCGAGGGGG 20

RESULT 11

AA09584
 ID AA09584 standard; DNA; 20 BP.

XX AA09584;

XX 26-SEP-2001 (first entry)

XX Immunoreactive CpG sequence-containing oligonucleotide #34.

XX CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.

XX Synthetic.

XX WO200151500-A1.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-US001122.

XX 14-JAN-2000; 2000US-0176115P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Klinman D, Ishii K, Verthelyi D;

XX WPI; 2001-442129/47.

XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.

XX Claim 5; Page 32; 48pp; English.

XX AA09551-AA09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The

CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumor cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematous and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria

XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGAGGGGG 20
 |||||
 DB 1 GGTGCATCGATCGAGGGGG 20

RESULT 12

AAS09588
 ID AAS09588 standard; DNA; 20 BP.

XX AAS09588;

26-SEP-2001 (first entry)

XX Immunoactive CpG sequence-containing oligonucleotide #38.

XX CpG sequence; immune response; non-B cell activation; interferon gamma;
 XX IFN-gamma; humoral; antibody production; interleukin-6 production;
 XX therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 XX bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 XX coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 XX hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 XX lupus erythematous; rheumatoid arthritis; multiple sclerosis;
 XX schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 XX Leishmania; Ebola; Anthrax; Listeria; ss.

XX Synthetic.

XX WO200151500-A1.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-US001122.

XX 14-JAN-2000; 2000US-0176115P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Klinman D, Ishii K, Verthelyi D;

XX WPI; 2001-442129/47.

XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.

PS Claim 5; Page 33; 48pp; English.

XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumor cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematous and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria

XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGAGGGGG 20

DB 1 GGTGCATCGATCGAGGGGG 20

RESULT 13

ABL35568

ID ABL35568 standard; DNA; 20 BP.

XX ABL35568;

04-APR-2002 (first entry)

XX Immunoactive CpG sequence-containing oligonucleotide SEQ ID NO: 494.

XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
 XX infection; allergy; cancer; hypersensitivity; bio-warfare;
 XX immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
 XX immunosuppressive; protozoicide; virucide; hepatotropic; gene therapy;
 XX antiinflammatory; antibacterial; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT misc_RNA 1..20

FT /tag= a

FT /note= "optionally thymidine is replaced by uracil to
 form RNA or DNA/RNA hybrids. Thymidine is linked to at
 least one other base through a ribose sugar"

XX WO200193902-A2.

XX 13-DEC-2001.

XX 07-JUN-2001; 2001WO-US018276.

XX 07-JUN-2000; 2000US-0209797P.

XX (BIOS-) BIOSYNEXUS INC.

XX Mond JJ, Flora M, Klinman DM;

```

XX New immunostimulatory compositions comprising RNA/DNA hybrid
PT oligonucleotides, useful for enhancing an immune response or inducing
PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT HIV infection.
XX
PS Example 11; Page 61; 68pp; English.
PS
XX The present invention relates to an immunostimulatory composition, which
CC comprises at least one oligonucleotide comprising both an RNA region and
CC a DNA region. The composition is useful for enhancing an immune response
CC or inducing cytokines. It can be used as a vaccine adjuvant and in
CC treating diseases, including pathogenic infection, (non-)malignant
CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC hepatitis, HIV or malaria. The composition is also useful for treating,
CC preventing or ameliorating the symptoms resulting from exposure to a bio-
CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC an immunostimulatory oligonucleotide described in the exemplification of
CC the invention
XX
XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATCGAGGGGG 20
Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 15
ABL35612
ID ABL35612 standard; DNA; 20 BP.
AC ABL35612;
XX
DT DT (first entry)
DE
XX Immunostimulatory oligonucleotide SEQ ID NO: 538.
XX
XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX infection; allergy; cancer; hypersensitivity; bio-warfare;
XX immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX antiinflammatory; antibacterial; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
XX misc_RNA 1..20
FT FT /*tag= a
FT FT /notes "optionally thymidine is replaced by uracil to
FT FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT FT least one other base through a ribose sugar"
XX
XX WO200193902-A2.
XX
XX 13-DEC-2001.
XX
XX 07-JUN-2001; 2001WO-US018276.
XX
XX 07-JUN-2000; 2000US-0209797P.
XX
XX (BIOS-) BIOSYNEXUS INC.
XX
XX Mond JJ, Flora M, Kliman DM;
XX
XX WPI; 2002-130570/17.
XX
XX New immunostimulatory compositions comprising RNA/DNA hybrid
PT

```

PT oligonucleotides, useful for enhancing an immune response or inducing
 PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
 PT HIV infection.
 XX

XX Example 11; Page 61; 68pp; English.

XX The present invention relates to an immunostimulatory composition, which
 CC comprises at least one oligonucleotide comprising both an RNA region and
 CC a DNA region. The composition is useful for enhancing an immune response
 CC or inducing cytokines. It can be used as a vaccine adjuvant and in
 CC treating diseases, including pathogenic infection, (non-)malignant
 CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
 CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
 CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
 CC hepatitis, HIV or malaria. The composition is also useful for treating,
 CC preventing or ameliorating the symptoms resulting from exposure to a bio-
 CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
 CC an immunostimulatory oligonucleotide described in the exemplification of
 CC the invention

XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCGAGGGGG 20
 Db 1 GGTGCATCGATGCGAGGGGG 20

Search completed: July 2, 2004, 08:31:32
 Job time : 151.878 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:09:30 ; Search time 31.3415 Seconds
(without alignments)
354.132 Million cell updates/sec

Title: US-10-068-160-1

Perfect score: 20

Sequence: 1 ggtgcacgacgagggggg 20

Scoring table: IDENTITY_MUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgm2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgm2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgm2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgm2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgm2_6/ptodata/2/ina/PCTUS_COMB.seq.*
- 6: /cgm2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.8	79.0	3358	3	US-09-248-571-2
2	15.8	79.0	3358	4	US-09-553-736-2
3	15.2	76.0	1584	4	US-09-252-981A-7138
4	15.2	76.0	1794	4	US-09-252-981A-7259
5	15.2	76.0	1872	4	US-09-252-981A-7359
6	14.8	74.0	622	3	US-09-125-030-45
7	14.4	72.0	759	4	US-09-252-991A-1486
8	14.4	72.0	1086	4	US-09-252-991A-13644
9	14.4	72.0	1092	4	US-09-252-991A-13444
10	14.4	72.0	1194	4	US-09-252-991A-13697
11	14.4	72.0	1308	4	US-09-252-991A-1592
12	14.4	72.0	1356	4	US-09-252-991A-1425
13	14.4	72.0	3591	4	US-09-252-991A-1690
14	14.4	72.0	4280	4	US-09-079-592-1
15	14.4	72.0	5496	4	US-09-462-284-1
16	14.4	72.0	32654	4	US-09-801-191A-3
17	14.4	72.0	1664976	4	US-08-916-4219-1
18	14.4	72.0	4403765	3	US-09-103-840A-2
19	14.4	72.0	4411529	3	US-09-103-840A-1
20	14.2	71.0	236	4	US-09-621-976-18710
21	14.2	71.0	339	4	US-09-107-532A-3414
22	14.2	71.0	589	1	US-08-454-196-3
23	14.2	71.0	589	3	US-09-064-033-3
24	14.2	71.0	589	4	US-09-291-046-3
25	14.2	71.0	1020	4	US-09-107-532A-1250
26	14.2	71.0	1029	2	US-08-743-637B-191
27	14.2	71.0	1128	4	US-09-107-532A-210

28	14.2	71.0	1140	1	US-08-454-196-1
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30	14.2	71.0	1140	4	US-09-291-046-1
31	14.2	71.0	1392	4	US-09-489-039A-4664
32	14.2	71.0	1607	4	US-09-328-857A-1
33	14.2	71.0	1627	1	US-08-615-170-2
34	14.2	71.0	1666	1	US-08-615-170-4
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36	14.2	71.0	2728	4	US-09-312-283C-213
37	14.2	71.0	2820	5	PCT-US93-11725-1
38	14.2	71.0	3842	4	US-09-976-594-279
39	14.2	71.0	4389	4	US-09-023-655-991
40	14.2	71.0	4726	4	US-09-598-401C-96
41	14.2	71.0	5581	4	US-09-023-655-966
42	14.2	71.0	28958	1	US-08-258-361B-6
43	14.2	71.0	28958	1	US-08-456-837-6
44	14.2	71.0	28958	1	US-08-457-342-6
45	14.2	71.0	28958	1	US-08-457-646A-6

ALIGNMENTS

RESULT 1
US-09-248-571-2
; Sequence 2, Application US/09248571
; Patent No. 6136539
; GENERAL INFORMATION:
; APPLICANT: BASBAUM, CAROL
; APPLICANT: GALLUP, MARIANNE
; APPLICANT: DAIZONG, LI
; APPLICANT: GEBREMICAHEL, ASSEFA
; APPLICANT: GENSCHE, ERIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITION OF MUC-5 MUCIN
; TITLE OF INVENTION: GENE EXPRESSION
; FILE REFERENCE: UCSF12/02
; CURRENT APPLICATION NUMBER: US/09/248,571
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: 60/074,398
; EARLIER FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3358
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-248-571-2

Query Match 79.0%; Score 15.8; DB 3; Length 3358;
Best Local Similarity 89.3%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 GTGCATCGATCGAGGGGG 20
Db 998 GTGCACCCATCGAGGGGG 1016

RESULT 2
US-09-553-736-2
; Sequence 2, Application US/09553736
; Patent No. 6440672
; GENERAL INFORMATION:
; APPLICANT: BASBAUM, CAROL
; APPLICANT: GALLUP, MARIANNE
; APPLICANT: DAIZONG, LI
; APPLICANT: GEBREMICAHEL, ASSEFA
; APPLICANT: GENSCHE, ERIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE INHIBITION OF MUC-5
; TITLE OF INVENTION: MUCIN GENE EXPRESSION
; FILE REFERENCE: UCSF-012/03US
; CURRENT APPLICATION NUMBER: US/09/553,736
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 09/248,571

Query Match 79.0%; Score 15.8; DB 4; Length 3358;
Best Local Similarity 89.5%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GTGCATCGATGACGGGGG 20
DB 998 GTGCACCATGACGGGGG 1016
RESULT 3
US-09-252-991A-7138/c
Sequence 7138, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7138
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7138

Query Match 76.0%; Score 15.2; DB 4; Length 1584;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTGCATCGATGACGGGGG 20
DB 1521 GGCGACGATGACGGGGTGG 1502
RESULT 4
US-09-252-991A-7259/c
Sequence 7259, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7259
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7259

Query Match 76.0%; Score 15.2; DB 4; Length 1794;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGTGCATCGATGACGGGGG 20
DB 208 GGCGACGATGACGGGGTGG 189

RESULT 5
US-09-252-991A-7359
Sequence 7359, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7359
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7359

Query Match 76.0%; Score 15.2; DB 4; Length 1872;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGTGCATCGATGACGGGGG 20
DB 271 GGCGACGATGACGGGGTGG 290

RESULT 6
US-09-129-030-46
Sequence 46, Application US/09129030A
Patent No. 6242221
GENERAL INFORMATION:
APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
TITLE OF INVENTION: GENOMIC PPO CLONES
FILE REFERENCE: 57072-PCT-US
CURRENT APPLICATION NUMBER: US/09/129,030A
CURRENT FILING DATE: 1998-08-04
EARLIER APPLICATION NUMBER: AU PN7856
EARLIER FILING DATE: 1996-02-05
EARLIER APPLICATION NUMBER: AU P02361
EARLIER FILING DATE: 1996-09-16
EARLIER APPLICATION NUMBER: PCT/AU97/00041
EARLIER FILING DATE: 1997-01-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 46
LENGTH: 622
TYPE: DNA
ORGANISM: RICE
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(300)
FEATURE:
NAME/KEY: CDS
LOCATION: (303)..(620)
US-09-129-030-46

Query Match 74.0%; Score 14.8; DB 3; Length 622;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGCATCGATGCAGGGG 19
 DB 217 GTGCATCGATGCAGGGG 234

RESULT 7
 US-09-252-991A-1486/c
 ; Sequence 1486, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 1486
 ; LENGTH: 759
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-1486

Query Match 72.0%; Score 14.4; DB 4; Length 759;
 Best Local Similarity 93.8%; Pred. No. 3.1e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCATCGATGCAGG 16
 DB 374 GGTGCATCGATGCAGG 359

RESULT 8
 US-09-252-991A-13644/c
 ; Sequence 13644, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 13644
 ; LENGTH: 1086
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-13644

Query Match 72.0%; Score 14.4; DB 4; Length 1086;
 Best Local Similarity 93.8%; Pred. No. 3.2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCATCGATGCAGGGG 19
 DB 264 GCATCGATGCAGGGG 249

RESULT 9
 US-09-252-991A-13444/c
 ; Sequence 13444, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 13444
 ; LENGTH: 1092
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-13444

Query Match 72.0%; Score 14.4; DB 4; Length 1092;
 Best Local Similarity 93.8%; Pred. No. 3.2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCATCGATGCAGGGG 19
 DB 305 GCATCGATGCAGGGG 290

RESULT 10
 US-09-252-991A-13697
 ; Sequence 13697, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 13697
 ; LENGTH: 1194
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-13697

Query Match 72.0%; Score 14.4; DB 4; Length 1194;
 Best Local Similarity 93.8%; Pred. No. 3.2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCATCGATGCAGGGG 19
 DB 971 GCATCGATGCAGGGG 986

RESULT 11
 US-09-252-991A-1592
 ; Sequence 1592, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142

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; SEQ ID NO 1592
; LENGTH: 1308
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1592

Query Match 72.0%; Score 14.4; DB 4; Length 1308;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGTCATCGATGCAGG 16
    |||||
Db 367 GGTGTCATCGATGCAGG 382

RESULT 12
US-09-252-991A-1425/c
; Sequence 1425, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1425
; TYPE: DNA
; LENGTH: 1356
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1425

Query Match 72.0%; Score 14.4; DB 4; Length 1356;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGTCATCGATGCAGG 16
    |||||
Db 981 GGTGTCATCGATGCAGG 966

RESULT 13
US-09-252-991A-1690
; Sequence 1690, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1690
; TYPE: DNA
; LENGTH: 3591
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1690

Query Match 72.0%; Score 14.4; DB 4; Length 3591;
Best Local Similarity 93.8%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGTCATCGATGCAGG 16
    |||||
Db 367 GGTGTCATCGATGCAGG 3730

us-10-068-160-1.rn1

Db 293 GGTGTCATCGATGCAGG 308

RESULT 14
US-09-079-592-1/c
; Sequence 1, Application US/09079592B
; Patent No. 666092
; GENERAL INFORMATION:
; APPLICANT: Alexander Blinkovsky
; APPLICANT: Kimberly Brown
; APPLICANT: Michael W. Rey
; APPLICANT: Alan Klotz
; APPLICANT: Tony Byun
; TITLE OF INVENTION: Polypeptides Having Dipeptidyl
; TITLE OF INVENTION: Aminopeptidase Activity And Nucleic Acids Encoding Same
; FILE REFERENCE: 5254,200-US
; CURRENT APPLICATION NUMBER: US/09/079,592B
; CURRENT FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 08/857,884
; PRIOR FILING DATE: 1997-05-16
; PRIOR APPLICATION NUMBER: 60/062,892
; PRIOR FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; TYPE: DNA
; LENGTH: 4280
; ORGANISM: Aspergillus
US-09-079-592-1

Query Match 72.0%; Score 14.4; DB 4; Length 4280;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGCATCGATGCAGGG 18
    |||||
Db 3367 TGCATCGATGCAGGG 3352

RESULT 15
US-09-462-284-1/c
; Sequence 1, Application US/09462284
; Patent No. 6309868
; GENERAL INFORMATION:
; APPLICANT: Nestec S.A.
; APPLICANT: Monod, Michel
; APPLICANT: Dumas, Agnes
; APPLICANT: Affolter, Micheal
; APPLICANT: Van Den Broek, Peter
; TITLE OF INVENTION: CLONING OF THE
; TITLE OF INVENTION: PROLYL-DIPEPTIDYL-PEPTIDASE FROM
; FILE REFERENCE: 8265-298
; CURRENT APPLICATION NUMBER: US/09/462,284
; CURRENT FILING DATE: 2000-01-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; TYPE: DNA
; LENGTH: 5496
; ORGANISM: Fungus
US-09-462-284-1

Query Match 72.0%; Score 14.4; DB 4; Length 5496;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGCATCGATGCAGGG 18
    |||||
Db 3745 TGCATCGATGCAGGG 3730
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Fri Jul 2 14:53:26 2004

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Job time : 38.3415 secs

us-10-068-160-1.rni

Page 5

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OM nucleic - nucleic search, using sw model

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(without alignments)
625.926 Million cell updates/sec

Title: US-10-068-160-1

Perfect score: 20

Sequence: 1 ggtgcacgacgagggggg 20

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Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	13	US-09-874-991C-494
2	20	100.0	20	13	US-09-874-991C-505
3	20	100.0	20	13	US-09-874-991C-538
4	20	100.0	20	15	US-10-068-160-1
5	20	100.0	20	15	US-10-068-160-54
6	20	100.0	20	15	US-10-194-035-32
7	20	100.0	20	15	US-10-194-035-34
8	20	100.0	20	15	US-10-194-035-37
9	20	100.0	20	15	US-10-194-035-38
10	20	100.0	20	15	US-10-194-035-43
11	20	100.0	20	15	US-10-194-035-72
12	20	100.0	20	17	US-10-666-022-176
13	20	100.0	20	17	US-10-666-022-177
14	20	100.0	22	13	US-09-874-991C-500

15	20	100.0	22	13	US-09-874-991C-544
16	20	100.0	28	13	US-09-874-991C-515
17	20	100.0	28	13	US-09-874-991C-527
18	20	100.0	29	13	US-09-874-991C-533
19	20	100.0	30	13	US-09-874-991C-521
20	20	100.0	30	13	US-09-874-991C-526
21	20	100.0	32	13	US-09-874-991C-463
22	19	95.0	19	15	US-10-194-035-53
23	19	95.0	19	15	US-10-194-035-73
24	18.4	92.0	20	13	US-09-874-991C-498
25	18.4	92.0	20	13	US-09-874-991C-499
26	18.4	92.0	20	13	US-09-874-991C-509
27	18.4	92.0	20	13	US-09-874-991C-510
28	18.4	92.0	20	13	US-09-874-991C-542
29	18.4	92.0	20	13	US-09-874-991C-543
30	18.4	92.0	20	15	US-10-068-160-7
31	18.4	92.0	20	15	US-10-068-160-11
32	18.4	92.0	20	15	US-10-068-160-21
33	18.4	92.0	20	15	US-10-068-160-30
34	18.4	92.0	20	15	US-10-068-160-35
35	18.4	92.0	20	15	US-10-068-160-37
36	18.4	92.0	20	15	US-10-068-160-52
37	18.4	92.0	20	15	US-10-068-160-53
38	18.4	92.0	20	15	US-10-068-160-64
39	18.4	92.0	20	15	US-10-068-160-65
40	18.4	92.0	20	15	US-10-194-035-40
41	18.4	92.0	20	15	US-10-194-035-81
42	18.4	92.0	20	15	US-10-194-035-82
43	18.4	92.0	20	15	US-10-194-035-100
44	18.4	92.0	20	15	US-10-194-035-101
45	18.4	92.0	20	15	US-10-194-035-104

ALIGNMENTS

RESULT 1
US-09-874-991C-494
; Sequence 494, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874.991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 494
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-494

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGACGGGGG 20
|||||
Db 1 GGTGCATCGATGACGGGGG 20

RESULT 2
US-09-874-991C-505
; Sequence 505, Application US/09874991C
; Publication No. US20040052763A1

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; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 505
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-505

Query Match          100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGACGGGGG 20
   |||||
Db 1 GGTGCATCGATCGACGGGGG 20

RESULT 3
US-09-874-991C-538
; Sequence 538, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 538
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-538

Query Match          100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGACGGGGG 20
   |||||
Db 1 GGTGCATCGATCGACGGGGG 20

RESULT 4
US-10-068-160-1
; Sequence 1, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, DENNIS
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
```

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; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-1

Query Match          100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGACGGGGG 20
   |||||
Db 1 GGTGCATCGATCGACGGGGG 20

RESULT 5
US-10-068-160-54
; Sequence 54, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, DENNIS
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-54

Query Match          100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGACGGGGG 20
   |||||
Db 1 GGTGCATCGATCGACGGGGG 20

RESULT 6
US-10-194-035-32
; Sequence 32, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, DENNIS
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
```

; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-32

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGAGGGGG 20

Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 7

US-10-194-035-34
; Sequence 34, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-34

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGAGGGGG 20

Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 8

US-10-194-035-37
; Sequence 37, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035

; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-37

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGAGGGGG 20

Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 9

US-10-194-035-38
; Sequence 38, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-38

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGAGGGGG 20

Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 10

US-10-194-035-43
; Sequence 43, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317

```
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-43

Query Match      100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATCGAGGGGG 20
   |||||
Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 11
US-10-194-035-72
; Sequence 72, Application US/10194035
; Publication No. US2003014429A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, DENNIS
; APPLICANT: VERTHELYI, DANIELA
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-72

Query Match      100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATCGAGGGGG 20
   |||||
Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 12
US-10-666-022-176
; Sequence 176, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: KLINMAN, DENNIS M.
; APPLICANT: VERTHELYI, DANIELA
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
```

```
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 176
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-666-022-176

Query Match      100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATCGAGGGGG 20
   |||||
Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 13
US-10-666-022-177
; Sequence 177, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: KLINMAN, DENNIS M.
; APPLICANT: VERTHELYI, DANIELA
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 177
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-666-022-177

Query Match      100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATCGAGGGGG 20
   |||||
Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 14
US-09-874-991C-500
; Sequence 500, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
```

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; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 500
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-500

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Query Match      100.0%; Score 20; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATGCAGGGGG 20
Db 3 GGTGCATCGATGCAGGGGG 22

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RESULT 15
US-09-874-991C-544
; Sequence 544, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 544
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-544

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```

Query Match      100.0%; Score 20; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATGCAGGGGG 20
Db 3 GGTGCATCGATGCAGGGGG 22

```

Search completed: July 2, 2004, 13:58:23
Job time : 155.146 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:38:45 ; Search time 1497.8 Seconds
(without alignments)
398.746 Million cell updates/sec

Title: US-10-068-160-1

Perfect score: 20

Sequence: 1 ggtgcacgatcagggggg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18.4	92.0	257	9	AV268287
2	17.4	87.0	240	9	AV281636
3	17.4	87.0	303	9	AV269637
4	17.4	87.0	473	12	BI507147

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C 5	17.4	87.0	1214	13	B0898390
C 6	17	85.0	541	28	B01614
C 7	17	85.0	807	13	CA101677
C 8	17	85.0	829	29	CG066914
C 9	16.8	84.0	272	13	EX639713
C 10	16.8	84.0	597	9	AV028453
C 11	16.8	84.0	631	12	BJ244833
C 12	16.8	84.0	638	9	AL692509
C 13	16.8	84.0	648	14	CB065500
C 14	16.8	84.0	671	12	BJ229325
C 15	16.8	84.0	671	14	CA920724
C 16	16.8	84.0	685	12	BJ634520
C 17	16.8	84.0	697	12	BJ250701
C 18	16.8	84.0	740	12	BJ617983
C 19	16.8	84.0	868	29	CG675673
C 20	16.8	84.0	927	12	BI733127
C 21	16.8	84.0	979	13	CA157988
C 22	16.8	84.0	1206	29	CG747404
C 23	16.4	82.0	245	10	AW325275
C 24	16.4	82.0	259	10	BB422123
C 25	16.4	82.0	277	28	AQ444154
C 26	16.4	82.0	374	14	CB966250
C 27	16.4	82.0	553	28	BH374854
C 28	16.4	82.0	584	13	BQ875411
C 29	16.4	82.0	621	28	BH450526
C 30	16.4	82.0	670	28	BH936954
C 31	16.4	82.0	679	28	BH577346
C 32	16.4	82.0	700	28	BH685253
C 33	16.4	82.0	702	28	BH471235
C 34	16.4	82.0	705	29	CB730492
C 35	16.4	82.0	712	13	BQ860936
C 36	16.4	82.0	738	28	BZ063097
C 37	16.4	82.0	747	28	BZ449138
C 38	16.4	82.0	815	14	CA766588
C 39	16.4	82.0	853	28	BZ449800
C 40	16.4	82.0	866	28	BH128747
C 41	16.4	82.0	915	29	CC588288
C 42	16.4	82.0	960	29	AG073881
C 43	16.4	82.0	1014	29	AG056417
C 44	16.4	82.0	1055	29	CNS05E18
C 45	16.4	82.0	1096	29	CNS05CFL

ALIGNMENTS

RESULT 1
AV268287

LOCUS
DEFINITION

musculus CDNA clone 4930534F16 3', mRNA sequence.

ACCESSION
AV268287

VERSION
AV268287.1

KEYWORDS
EST.

SOURCE
Mus musculus (house mouse)

REFERENCE
1 (bases 1 to 257)

AUTHORS
Konno, H., Aizawa, K., Akabira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, I., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, K., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Takahashi, F., Tateo, M., Tomimaga, N., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, I., Yoshiki, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.

RIKEN Mouse ESTs (Konno, H., et al. 1999)

Unpublished (1999)

CONTACT: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

AV268287 257 bp mRNA linear EST 05-NOV-1999
musculus CDNA clone 4930534F16 3', mRNA sequence.

AV268287 257 bp mRNA linear EST 05-NOV-1999
musculus CDNA clone 4930534F16 3', mRNA sequence.

AV268287.1 GI:6256324
Mus musculus (house mouse)

AV268287 257 bp mRNA linear EST 05-NOV-1999
musculus CDNA clone 4930534F16 3', mRNA sequence.

AV268287 257 bp mRNA linear EST 05-NOV-1999
musculus CDNA clone 4930534F16 3', mRNA sequence.

AV268287 257 bp mRNA linear EST 05-NOV-1999
musculus CDNA clone 4930534F16 3', mRNA sequence.

AV268287 257 bp mRNA linear EST 05-NOV-1999
musculus CDNA clone 4930534F16 3', mRNA sequence.

AV268287 257 bp mRNA linear EST 05-NOV-1999
musculus CDNA clone 4930534F16 3', mRNA sequence.

AV268287 257 bp mRNA linear EST 05-NOV-1999
musculus CDNA clone 4930534F16 3', mRNA sequence.

AV268287 257 bp mRNA linear EST 05-NOV-1999
musculus CDNA clone 4930534F16 3', mRNA sequence.

AV268287 257 bp mRNA linear EST 05-NOV-1999
musculus CDNA clone 4930534F16 3', mRNA sequence.

AV268287 257 bp mRNA linear EST 05-NOV-1999
musculus CDNA clone 4930534F16 3', mRNA sequence.

AV268287 257 bp mRNA linear EST 05-NOV-1999
musculus CDNA clone 4930534F16 3', mRNA sequence.

AV268287 257 bp mRNA linear EST 05-NOV-1999
musculus CDNA clone 4930534F16 3', mRNA sequence.

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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp/
URL: http://genome.gsc.riken.go.jp/
Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,
Matsuura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and
Hayashizaki, Y.
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh, M., Kitsuunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

FEATURES

Location/Qualifiers
1..257
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4930534F16"
/sex="male"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male testis
(DH10B)"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGATCTCGAGTTAATTAATTAATCCCCCCCCC 3']. cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGATCTCGAGTTAATTAATTAATCCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I. Cloning sites, 5' end: Sali; 3' end: BamHI."

ORIGIN

Query Match 92.0%; Score 18.4; DB 9; Length 257;
Best Local Similarity 95.0%; Pred. No. 7.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTGTCATCGATCGAGGGGG 20
|||||
DB 95 GGTGTCATCGAGCGGGGG 114
|||||
RESULT 2
AV281636 240 bp mRNA linear EST 05-NOV-1999
LOCUS AV281636 RIKEN full-length enriched, adult male testis (DH10B) Mus
DEFINITION musculus cDNA clone 4930534F16, mRNA sequence.
ACCESSION AV281636
VERSION AV281636.1 GI:6269673
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 240)
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I.,
Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K.,
Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Suzuki, H., Takahashi, P., Tateno, M., Tomimaga, N.,
Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A.,
Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Konno, H., et al. 1999)
Unpublished (1999)

TITLE

CONTACT: Yoshinori Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp/
URL: <http://genome.gsc.riken.go.jp/>
Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,
Matsuura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and
Hayashizaki, Y.

Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh, M., Kitsuunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

FEATURES

Location/Qualifiers
1..240
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4933425J05"
/sex="male"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male testis
(DH10B)"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGATCTCGAGTTAATTAATTAATCCCCCCCCC 3']. cDNA
was prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGATCTCGAGTTAATTAATTAATCCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I. Cloning sites, 5' end: Sali; 3' end: BamHI."

ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 240;
Best Local Similarity 94.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/clone lib="Bee Brain Normalized/Subtracted Library, BB17"
 /note="Organ: Brain; Vector: pVT3-Pac; Site: 1; EcoRI;
 Site: 2; NotI; This BB17 cDNA library was generated by
 subtraction of the BB16 library with 4000 previously
 sequenced clones. The BB16 library was contributed by the
 Soares laboratory and it was constructed and normalized
 as described by Bonaldo, M.F., Lennon, G. and Soares,
 M.B. (1996). Genome Research 6(9): 791-806. RNA was
 prepared from dissected brains of adult worker bees of
 various ages and various behavioral groups."

ORIGIN

Query Match 87.0%; Score 17.4; DB 12; Length 473;
 Best Local Similarity 94.7%; Pred. No. 2.4e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTGATCGATCGAGGGG 19
 |||||
 Db 336 GGTGATCGAGCGGGG 318

RESULT 5

BQ898390/c
 LOCUS
 DEFINITION 1214 bp mRNA linear EST 16-AUG-2002
 AGENCOURT_8712137 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6295181
 5', mRNA sequence.
 ACCESSION BQ898390
 VERSION BQ898390.1 GI:22290404
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@email.nih.gov

Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2501 row: a column: 06
 High quality sequence stop: 150.

FEATURES

source

Location/Qualifiers
 1..1214
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6295181"
 /tissue_type="melanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 112"
 /note="Organ: skin; Vector: pOT37; Site: 1; XhoI; Site: 2;
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GCCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 87.0%; Score 17.4; DB 13; Length 1214;
 Best Local Similarity 94.7%; Pred. No. 3.2e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTGATCGATCGAGGGG 19
 |||||

Db 301 GGTGACCGATCGAGGGG 283

RESULT 6

B01614/c
 LOCUS
 DEFINITION 541 bp DNA linear GSS 13-JUL-1996
 CSRL-134g10-u CSRL flow sorted Chromosome 11 specific cosmid Homo
 sapiens genomic clone CSRL-134g10, genomic survey sequence.

ACCESSION B01614
 VERSION B01614.1 GI:1410892
 KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 541)
 Evans, G.A., Burbee, D., Davies, C., Hahner, L., Oliver, T., Gilbert, M.,
 Jones, D., Ward, T., Gillilan, E., Schagemann, J., Probst, S.,
 Harris, J., DeFord, J., McFarland, J., Burzinski, K., Khan, M.,
 Kupfer, K. and Garner, H.R.
 Genomic Sequence Sampled Map of Chromosome 11

TITLE

JOURNAL Unpublished (1996)

COMMENT

Contact: Evans GA, Shane Probst
 McDermott Center for Human Growth and Development
 University of Texas Southwestern Medical Center At Dallas
 5323 Harry Hines Blvd, Dallas TX 75235-8591
 Tel: 214-648-1600
 Fax: 214-648-1666

Email: gevaus@utsw.swmed.edu, shane@mcdermott.swmed.edu

PCR Primers

FORWARD: TACTAAGCGAGCTAGCTG

BACKWARD: TTGGACGATTAGCTCAG

Seq primer: T7

Class: cosmid ends

High quality sequence stop: 541.

FEATURES

source

Location/Qualifiers
 1..541
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="CSRL-134g10"
 /sex="female"
 /cell_type="chimeric hamster somatic cell hybrid"
 /clone_lib="CSRL flow sorted Chromosome 11 specific
 cosmid"
 /note="vector: sCos-1; Human Chromosome 11 specific cosmid
 library prepared from flow sorted human Chromosome 11
 derived from Chinese Hamster Ovary (CHO) monochromosomal
 somatic cell hybrid, J1"

ORIGIN

Query Match 85.0%; Score 17; DB 28; Length 541;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGATCGATCGAGGG 17
 |||||

Db 181 GGTGATCGATCGAGGG 165
 |||||

RESULT 7

CA101677/c
 LOCUS
 DEFINITION 807 bp mRNA linear EST 23-SEP-2003
 SCACHR1040C03.g HRI Saccharum officinarum cDNA clone SCACHR1040C03
 5', mRNA sequence.

ACCESSION CA101677

VERSION CA101677.1 GI:34954984

KEYWORDS EST.

SOURCE Saccharum officinarum

ORGANISM Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 clade; Panicoideae; Andropogoneae; Saccharum.

```

REFERENCE
1 (bases 1 to 807)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccnet.fvav.unesp.br
Plate: 040 row: C column: 03
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1 .807
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCACHRI040C03"
/lab_host="DH10B"
/clone_lib="HRI"
/notes="Organ: seedlings inoculated with Herbaspirillum
rubisubalbicans; Vector: pSport1; Site 1: SalI; Site 2:
NotI; An unidirectional cDNA library generated from
[seedlings inoculated with Herbaspirillum
rubisubalbicans]. cDNA was prepared from poly(A+ mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://succest.lad.ic.unicamp.br/public"

ORIGIN
Query Match 85.0%; Score 17; DB 13; Length 807;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCATCGATGCAGGGGG 20
|||||
DB 32 GCATCGATGCAGGGGG 16

RESULT 8
CG066914/c
LOCUS
DEFINITION
PUBJ87TD ZM 0.6_1.0 KB Zea mays genomic clone ZMWBTa0544P06,
genomic survey sequence.
ACCESSION
CG066914
VERSION
CG066914.1 GI:33939094
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 839)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Reinick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUBJ87TB
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP

FEATURES
source
Class: sheared ends.
Location/Qualifiers
1 .839
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMWBTa0544P06"
/clone_lib="ZM 0.6_1.0 KB"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
cot selected genomic DNA library"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTGCATCGATGCAGGGG 18
|||||
DB 124 GTGCATCGATGCAGGGG 108

RESULT 9
BX639713/c
LOCUS
DEFINITION
BX639713 pBluescript Lion Mus musculus cDNA clone LIONP462H0719 3',
mRNA sequence.
ACCESSION
BX639713
VERSION
BX639713.1 GI:33619588
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 272)
Henrich,J., Hermanns,J., Kranz,H., Loebbert,R., Schluter,T.,
Schuette,D., Weindel,M., Heil,O., Ebert,L., Neubert,P., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
Mouse ArrayTAG cDNA (LION)
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; LIONP462H0719.
RZPDLIB;
http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi?response?libNo=4
G2 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
RP: CAGGAACAGCTATGAC.
Location/Qualifiers
1 .272
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="LIONP462H0719"
/lab_host="DH10B"
/clone_lib="pBluescript Lion"

ORIGIN
Query Match 84.0%; Score 16.8; DB 13; Length 272;
Best Local Similarity 90.0%; Pred. No. 3.8e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCATCGATGCAGGGGG 20
|||||
DB 168 GGTCCTCGAGGCAGGGGG 149

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```

RESULT 10
AV028453
LOCUS
DEFINITION
AV028453 Mus musculus adult C57BL/6J Brain Mus musculus cDNA clone
1432000GLJ3, mRNA sequence.
AV028453
VERSION
AV028453.1 GI:4783418
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 597)
Carinci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T.,
Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M.,
Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H.,
Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y.,
Sugahara, Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y.,
Tomimaga, N., Watanabe, S., Yagane, M., Yamamura, T., Yokota, T.,
Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
FEATURES
source
Location/Qualifiers
1..597
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1432000GLJ3"
/sex="male"
/tissue_type="brain"
/dev_stage="adult"
/clone_lib="Mus musculus adult C57BL/6J brain"
ORIGIN
Query Match 84.0%; Score 16.8; DB 9; Length 597;
Best Local Similarity 90.0%; Pred. No. 4.7e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGTGCATCGATCGAGGGGG 20
|||||
DB 64 GTGCATCGATCGAGGGGG 83
|||||
RESULT 11
BJ244833/c
LOCUS
DEFINITION
BJ244833 Y. Ogihara unpublished cDNA library, Wh_f Triticum
aestivum cDNA clone whf16m07 5', mRNA sequence.
BJ244833
VERSION
BJ244833.1 GI:20057113
SOURCE
Triticum aestivum (bread wheat)
ORGANISM
Triticum aestivum
REFERENCE
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

```

```

Poolidae; Triticeae; Triticum.
1 (bases 1 to 631)
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadasi Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
source
Location/Qualifiers
1..631
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whf16m07"
/tissue_type="spike at flowering date"
/dev_stage="peak", scale 10.5.1"
/clone_lib="Y. Ogihara unpublished cDNA library, Wh_f"
ORIGIN
Query Match 84.0%; Score 16.8; DB 12; Length 631;
Best Local Similarity 90.0%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGTGCATCGATCGAGGGGG 20
|||||
DB 559 GTGCATCGAGAGGGGG 540
|||||
RESULT 12
AL692509
LOCUS
DEFINITION
AL692509 NAH Anopheles gambiae cDNA clone NAH-P05-H-10-5, mRNA
sequence.
ACCESSION
AL692509
VERSION
AL692509.1 GI:19612418
KEYWORDS
EST...
SOURCE
Anopheles gambiae (African malaria mosquito)
ORGANISM
Anopheles gambiae
REFERENCE
1 (bases 1 to 638)
Christophides, G.K., Blass, K., Zdobnov, E.M., Carmouch, R., Benes, V.
and Karatos, F.C.
Unpublished (2002)
Contact: Christophides GK
Fotis C. Kafatos Laboratory
European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, Germany
Tel: +49 6221 387-440
Fax: +49 6221 387-306
Email: christop@embl-heidelberg.de
Plate: P05 row: H column: 10.
FEATURES
source
Location/Qualifiers
1..638
/organism="Anopheles gambiae"
/mol_type="mRNA"
/db_xref="taxon:7165"
/clone="NAH-P05-H-10-5"
/lab_host="E. coli DH10B"
/clone_lib="NAH"
/notes="vector: pT7T3D-Pac (Pharmacia); Site 1: NotI;
Site 2: EcoRI; ESTs sequenced from the T7 priming site
that reads from the 5' end of cDNA. The NAH1 is a
directionally cloned and normalized, oligo-r primed cDNA
library constructed from heads of Anopheles gambiae
according to: Bonaldo, Lennon & Soares (1996);

```

Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery, Genome Research 6, 791-806.

```

ORIGIN
      Query Match      84.0%; Score 16.8; DB 9; Length 638;
      Best Local Similarity 90.0%; Pred.No. 4.8e+03;
      Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GGTCATCGATCGAGGGGG 20
          |||||
Db       212  GGTCGAACGATCGAGGGG 231
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```

RESULT 13	
CB065500/c	
LOCUS	648 bp mRNA linear EST 21-JAN-2003
DEFINITION	EST645181 HOGA Medicago truncatula cDNA clone HOGA-19K1, mRNA
ACCESSION	CB065500
VERSION	CB065500.1
KEYWORDS	GI:27811078
SOURCE	EST.
ORGANISM	Medicago truncatula (barrel medic)
	Medicago truncatula
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	Rosids; eurosoids I; Fabales; Papilionoideae; Trifolieae;
	Medicago.

REFERENCE	1 (bases 1 to 648)
AUTHORS	Hahn, M.G., Ojanen-Reuhs, T., Samac, D., Town, C.D., Van Aken, S., Uhrback, T., Cho, J. and Fraser, C.M.
TITLE	ESTs from roots of <i>Medicago truncatula</i> treated with oligolacturonides of DP 6-20
JOURNAL	Unpublished (2001)
COMMENT	Contact: Michael G. Hahn Complex Carbohydrate Research Center University of Georgia 220 Riverbend Road, Athens, GA 30602-4712, USA Tel: 706-542-4457 Fax: 706-542-4412 Email: hahn@ccrc.uga.edu TIGR sequence name: MTWCU51TV More information is available at: www.medicago.org Seq primer: (gta ata cga ctc act ata ggg c).

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        /tissue_type="3 day old seedling roots"
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        /clone_lib="HOGA"
        /note="vector: pluscript SK-; Site 1: EcoRI; Site 2:
        XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
        was directionally ligated into the Unizap XR vector from
        Stratagene and packaged using Gigapack III Gold packaging
        extracts. Plasmids containing cDNA inserts were excised
        from the recombinant lambda-zap phage using Ex-assist
        helper phage and propagated in SOLR cells."

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ORIGIN

Query Match	84.0%	Score 16.8;	DB 14;	Length 648;
Best Local Similarity	90.0%;	Pred. No. 4.9e+03;		
Matches 18;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

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445 GGTGCATCGTTGCAGTGGG 426

RESULT 14	ACCESSION
BJ229325	VERSION
LOCUS	KEYWORDS
DEFINITION	SOURCE
	ORGANISM

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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3				
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FEATURES

ORIGIN

Query Match 84.0%; Score 16.8; DB 12; Length 671;
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RESULT 15	ACCESSION	ORGANISM
CA920724/c	VERSION	
LOCUS	KEYWORDS	
DEFINITION	SOURCE	

REFERENCE AUTHORS	TITLE	JOURNAL COMMENT
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86
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90
91
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93
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96
97
98
99
100

JOURNAL
COMMENT

University of Minnesota
220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvanden@cbs.umn.edu

Fax: 612 623 1738
Email: kvandenb@cbs.umn.edu

BJ229325 671 bp mRNA linear EST 05-APR-2002
 BJ229325 Y. Ogiwara unpublished cDNA library, WdL Triticum
 aestivum cDNA clone wdh119e17 3', mRNA sequence.
 BJ229325
 BJ229325 BJ229325.1 GI:20048595
 EST.
 Triticum aestivum (bread wheat)
 Triticum aestivum
 Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooidae; Triticeae; Triticum.

1 (bases 1 to 671)
Ogihara, Y. and Murai, K.
Expressed genes in *Triticum aestivum*
Unpublished (2002)
Contact: Tadasu Shin-i

Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsbini@genes.nig.ac.jp

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1. 671
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/dev_stages="Feekes' scale 1"
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Query Match 84.0%; Score 16.8; DB 12; Length 671;
Best Local Similarity 90.0%; Pred. No. 4.9e+03;
Matches 18: Conservative 0; Mismatches 2; Indels 0

CA920724 571 bp mRNA linear EST 09-MAY-2003
EST638442 MTUS Medicago truncatula cDNA clone MTUS-31C10, mRNA
sequence.

EST.
Medicago truncatula (barrel medic)
Medicago truncatula
Eukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

1 (bases 1 to 671)
VandenBosch,K., Endre,G., Silverstein,K, Town,C.D., Van Aken,S.,
Utterback,T., Cheung,F. and Fraser,C.M.
The *Medicago truncatula* 6K unigene set: cDNA clones selected and
re-arrayed from various libraries

Unpublished (2002)
Contact: Vanderschorsch K
Department of Plant Biology
Department of Minnesota
220 Biological Center, 1445 Gortner Ave., St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandersorb@bbs.umn.edu

Fax: 612 623 1738
Email: kvandenb@cbs.umn.edu

TV plate 31 rotated 180 degrees at TIGR
TIGR sequence name: MTUS63TV
More information is available at: www.medicago.org
Seq primer: (gtA ATA CgA Ctc Act ATA 999 C).

FEATURES

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/clone_lib="MTUS"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant Lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."

ORIGIN

Query Match 84.0%; Score 16.8; DB 14; Length 671;
Best Local Similarity 90.0%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGTGCATCGATGCAGCGGG 20
Db 376 GGTGCATCGTTGCGTGGG 357

Search completed: July 2, 2004, 13:32:50
Job time : 1502.92 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:36:05 ; Search time 704.146 Seconds
(without alignments)
1231.080 Million cell updates/sec

Title: US-10-068-160-2
Perfect score: 20
Sequence: 1 ggtgacccggtagcagggggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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41: em_hgt_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	20	6	AX194442 Sequence
2	20	100.0	20	6	AX352200 Sequence
3	20	100.0	20	6	AX352208 Sequence
4	20	100.0	20	6	AX352211 Sequence
5	20	100.0	20	6	AX352218 Sequence
6	20	100.0	20	6	AX352244 Sequence
7	20	100.0	20	6	AX465392 Sequence
8	20	100.0	28	6	AX352221 Sequence
9	20	100.0	28	6	AX352229 Sequence
10	20	100.0	28	6	AX352233 Sequence
11	20	100.0	28	6	AX352241 Sequence
12	20	100.0	40	6	AX352252 Sequence
13	18.4	92.0	20	6	AX194501 Sequence
14	18.4	92.0	20	6	AX194501 Sequence
15	18.4	92.0	20	6	AX352203 Sequence
16	18.4	92.0	20	6	AX352210 Sequence
17	18.4	92.0	20	6	AX352214 Sequence
18	18.4	92.0	20	6	AX352247 Sequence
19	18.4	92.0	28	6	AX352220 Sequence
20	18.4	92.0	28	6	AX352232 Sequence
21	18.4	92.0	28	6	AX352236 Sequence
22	18.4	92.0	28	6	AX352242 Sequence
23	17.4	87.0	19	6	AX194422 Sequence
24	17.4	87.0	155724	4	AX465372 Sequence
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26	17.4	87.0	187364	10	AL592465 Mouse DNA
27	17.4	87.0	238358	10	AL592465 Mouse DNA
28	17.4	87.0	260424	2	AC131745 Mus muscu
29	17.4	87.0	307820	2	AC130831 Mus muscu
30	17.4	87.0	307820	2	AC130831 Mus muscu
31	17	85.0	10782	1	AE001002 Archaeogl
32	17	85.0	138859	9	AL359076 Human DNA
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36	16.8	84.0	20	6	AX194438 Sequence
37	16.8	84.0	20	6	AX194443 Sequence
38	16.8	84.0	20	6	AX194472 Sequence
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41	16.8	84.0	20	6	AX352198 Sequence
42	16.8	84.0	20	6	AX352209 Sequence
43	16.8	84.0	20	6	AX352242 Sequence
44	16.8	84.0	20	6	AX465382 Sequence
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ALIGNMENTS

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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AX194442
Sequence 42 from Patent WO0151500.
AX194442
AX194442.1 GI:15385098

synthetic construct
synthetic construct
artificial sequences.

1
Klinman,D., Ishii,K. and Verthelyi,D.
Oligodeoxynucleotide and its use to induce an immune response
Patent: WO 0151500-A 42 19-JUL-2001.
Secretary of the Department of Health and Human Services (US)

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1 GGTGCACCGGTGCAGGGGG 20

RESULT 2
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DEFINITION
  Sequence 496 from Patent WO0193902.
ACCESSION
  AX352200
VERSION
  AX352200.1 GI:18617483
KEYWORDS
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SOURCE
  synthetic construct
  synthetic construct
  artificial sequences.
ORGANISM
  1
REFERENCE
  1
  AUTHORS
    Mond, J.J., Flora, M. and Klinman, D.M.
  TITLE
    Immunostimulatory rna/dna hybrid molecules
  JOURNAL
    Patent: WO 0193902-A 496 13-DEC-2001;
    Biosynexus Incorporated (US)
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        /organism="synthetic construct"
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DEFINITION
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ACCESSION
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VERSION
  AX352208.1 GI:18617491
KEYWORDS
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SOURCE
  synthetic construct
  synthetic construct
  artificial sequences.
ORGANISM
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REFERENCE
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  AUTHORS
    Mond, J.J., Flora, M. and Klinman, D.M.
  TITLE
    Immunostimulatory rna/dna hybrid molecules
  JOURNAL
    Patent: WO 0193902-A 504 13-DEC-2001;
    Biosynexus Incorporated (US)
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ORGANISM
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REFERENCE
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  AUTHORS
    Mond, J.J., Flora, M. and Klinman, D.M.
  TITLE
    Immunostimulatory rna/dna hybrid molecules
  JOURNAL
    Patent: WO 0193902-A 507 13-DEC-2001;
    Biosynexus Incorporated (US)
FEATURES
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RESULT 5
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DEFINITION
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ACCESSION
  AX352218
VERSION
  AX352218.1 GI:18617501
KEYWORDS
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SOURCE
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ORGANISM
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REFERENCE
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  AUTHORS
    Mond, J.J., Flora, M. and Klinman, D.M.
  TITLE
    Immunostimulatory rna/dna hybrid molecules
  JOURNAL
    Patent: WO 0193902-A 514 13-DEC-2001;
    Biosynexus Incorporated (US)
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  AUTHORS
    Mond, J.J., Flora, M. and Klinman, D.M.
  TITLE
    Immunostimulatory rna/dna hybrid molecules
  JOURNAL
    Patent: WO 0193902-A 514 13-DEC-2001;
    Biosynexus Incorporated (US)
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LOCUS
DEFINITION    Sequence 540 from Patent WO0193902.
ACCESSION     AX352244
VERSION       AX352244.1  GI:18617527
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      artificial sequences.

REFERENCE
AUTHORS       Mond, J.J., Flora, M. and Klinman, D.M.
TITLE         Immunostimulatory rna/dna hybrid molecules
JOURNAL       Patent: WO 0193902-A 540 13-DEC-2001;
              Biosynexus Incorporated (US)
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Db 1 GGTGCACCGGTGCAGGGGGG 20

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DEFINITION    Sequence 60 from Patent WO0211761.
ACCESSION     AX465392
VERSION       AX465392.1  GI:21899755
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      artificial sequences.

REFERENCE
AUTHORS       Mond, J.J., Prince, G. and Klinman, D.M.
TITLE         Vaccine against RSV
JOURNAL       Patent: WO 0211761-A 60 14-FEB-2002;
              HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
              MEDICINE (US)
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ORIGIN
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ACCESSION     AX352221
VERSION       AX352221.1  GI:18617504
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      artificial sequences.

REFERENCE
AUTHORS       Mond, J.J., Flora, M. and Klinman, D.M.
TITLE         Immunostimulatory rna/dna hybrid molecules
JOURNAL       Patent: WO 0193902-A 529 13-DEC-2001;
              Biosynexus Incorporated (US)
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
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RESULT 10
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DEFINITION    Sequence 529 from Patent WO0193902.
ACCESSION     AX352233
VERSION       AX352233.1  GI:18617516
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SOURCE        synthetic construct
ORGANISM      artificial sequences.

REFERENCE
AUTHORS       Mond, J.J., Flora, M. and Klinman, D.M.
TITLE         Immunostimulatory rna/dna hybrid molecules
JOURNAL       Patent: WO 0193902-A 529 13-DEC-2001;
              Biosynexus Incorporated (US)
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGGG 20
    |||||
Db 1 GGTGCACCGGTGCAGGGGGG 20

RESULT 9
AX352229
LOCUS
DEFINITION    Sequence 525 from Patent WO0193902.
ACCESSION     AX352229
VERSION       AX352229.1  GI:18617512
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      artificial sequences.

REFERENCE
AUTHORS       Mond, J.J., Flora, M. and Klinman, D.M.
TITLE         Immunostimulatory rna/dna hybrid molecules
JOURNAL       Patent: WO 0193902-A 525 13-DEC-2001;
              Biosynexus Incorporated (US)
FEATURES
source        1. .28
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Synthetic HDR"

ORIGIN
Query Match   100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGGG 20
    |||||
Db 1 GGTGCACCGGTGCAGGGGGG 20

RESULT 10
AX352233
LOCUS
DEFINITION    Sequence 529 from Patent WO0193902.
ACCESSION     AX352233
VERSION       AX352233.1  GI:18617516
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      artificial sequences.

REFERENCE
AUTHORS       Mond, J.J., Flora, M. and Klinman, D.M.
TITLE         Immunostimulatory rna/dna hybrid molecules
JOURNAL       Patent: WO 0193902-A 529 13-DEC-2001;
              Biosynexus Incorporated (US)
FEATURES
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              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Synthetic HDR"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGGG 20
    |||||
Db 1 GGTGCACCGGTGCAGGGGGG 20
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
|||||
Db 9 GGTGCACCGGTGCAGGGGG 28

RESULT 11

AX352241
LOCUS AX352241 28 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 537 from Patent WO0193902.
ACCESSION AX352241
VERSION AX352241.1 GI:18617524
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mond, J.J., Flora, M. and Klimman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 537 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
source Location/Qualifiers
1..28
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
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Db 9 GGTGCACCGGTGCAGGGGG 28

RESULT 12

AX352252
LOCUS AX352252 40 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 548 from Patent WO0193902.
ACCESSION AX352252
VERSION AX352252.1 GI:18617535
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mond, J.J., Flora, M. and Klimman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 548 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
|||||
Db 14 GGTGCACCGGTGCAGGGGG 33

RESULT 13

AX194501
LOCUS AX194501 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 101 from Patent WO0151500.
ACCESSION AX194501
VERSION AX194501.1 GI:15385157
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE

1
AUTHORS Klinman, D., Ishii, K. and Verthelyi, D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 101 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA"

ORIGIN

Query Match 92.0%; Score 18.4; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 7.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
|||||
Db 1 GGTGCACCGGTGCAGGGGG 20

RESULT 14

AX352199
LOCUS AX352199 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 495 from Patent WO0193902.
ACCESSION AX352199
VERSION AX352199.1 GI:18617482
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mond, J.J., Flora, M. and Klimman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 495 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"

ORIGIN

Query Match 92.0%; Score 18.4; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 7.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
|||||
Db 1 GGTGCACCGGTGCAGGGGG 20

RESULT 15

AX352203
LOCUS AX352203 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 499 from Patent WO0193902.

```

ACCESSION AX352203
VERSION AX352203.1 GI:18617486
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
         artificial sequences.
REFERENCE 1
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 499 13-DEC-2001;
        Biosynexus Incorporated (US)
FEATURES
    source
        1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic HDR"
ORIGIN
    Query Match          92.0%; Score 18.4; DB 6; Length 20;
    Best Local Similarity 95.0%; Pred. No. 7.6e+02;
    Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTCACGGGGG 20
   |||||
Db 1 GGTGCACCGGTCACGGGGG 20

Search completed: July 2, 2004, 10:07:55
Job time : 705.146 secs

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Result No.	Query §		DB	ID	Description
	Score	Match			
1	20	100.0	20	4 AAC80622	Immunogen
2	20	100.0	20	4 AAS09592	Immunorea
3	20	100.0	20	6 ABL35614	Immunosti
4	20	100.0	20	6 ABL35578	Immunosti
5	20	100.0	20	6 ABL35581	Immunosti
6	20	100.0	20	6 ABL35570	Immunosti
7	20	100.0	20	6 ABL35588	Immunosti
8	20	100.0	20	6 ABK46470	Immunosti
9	20	100.0	20	7 ACC48296	Cpg oligo
10	20	100.0	20	7 ACC48313	Cpg oligo
11	20	100.0	20	8 ACC83118	D class C
12	20	100.0	20	8 ACC83152	D class C
13	20	100.0	20	9 ADD01049	Cpg D oli
14	20	100.0	28	6 ABL35599	Immunosti
15	20	100.0	28	6 ABL35603	Immunosti
16	20	100.0	28	6 ABL35591	Immunosti
17	20	100.0	28	6 ABL35611	Immunosti
18	20	100.0	40	6 ABL35622	Immunosti
19	18.4	92.0	20	4 AAS09651	Immunorea
20	18.4	92.0	20	6 ABL35573	Immunosti
21	18.4	92.0	20	6 ABL35584	Immunosti
22	18.4	92.0	20	6 ABL35569	Immunosti
23	18.4	92.0	20	6 ABL35617	Immunosti

CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
 CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 CC -3'. The central CpG motif is unmetlylated, and the oligonucleotides
 CC optionally have phosphorothioate linkages which make them more resistant
 CC to degradation. The invention also relates to an oligonucleotide delivery
 CC complex comprising an oligonucleotide of the invention and a targeting
 CC agent, and a pharmaceutical composition comprising the oligonucleotide
 CC delivery complex. The oligonucleotides are able to induce either a cell-
 CC mediated (n-cell) response or a humoral (B-cell, antibody) response, with
 CC oligonucleotides of the sequence 5'-RY-CpG-RY-3', being able to induce a
 CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3',
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g., macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergenic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic
 CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antisense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention
 XX
 SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTGCACCGGTGCAGGGGG 20
 Db 1 GGTGCACCGGTGCAGGGGG 20
 RESULT 2
 AAS09592
 ID AAS09592 standard; DNA; 20 BP.
 XX
 AC AAS09592;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Immunoreactive CpG sequence-containing oligonucleotide #42.
 XX
 KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.
 XX
 OS Synthetic.
 XX
 PN WO200151500-A1.
 XX
 XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-US001122.
 XX
 PR 14-JAN-2000; 2000US-0176115P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Klinman D, Ishii K, Verthelyi D;
 XX
 XX WPI; 2001-442129/47.
 XX
 PS Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.
 XX
 XX Claim 5; Page 34; 48pp; English.
 XX
 CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria
 XX
 SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTGCACCGGTGCAGGGGG 20
 Db 1 GGTGCACCGGTGCAGGGGG 20
 RESULT 3
 ABL35614
 ID ABL35614 standard; DNA; 20 BP.
 XX
 AC ABL35614;
 XX
 DT 04-APR-2002 (first entry)
 XX
 DE Immunostimulatory oligonucleotide SEQ ID NO: 540.
 XX
 KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
 KW infection; allergy; cancer; hypersensitivity; bio-warfare;
 KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
 KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
 KW antiinflammatory; antibacterial; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 XX misc_RNA 1..20
 FT

```

FT      /*tag= a
FT      /note= "optionally thymidine is replaced by uracil to
FT      form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT      least one other base through a ribose sugar"
XX
XX
XX      WO200193902-A2.
XX
XX      13-DEC-2001.
XX
XX      07-JUN-2001; 2001WO-US018276.
XX
XX      07-JUN-2000; 2000US-0209797P.
XX
XX      (BIOS-) BIOSYNEXUS INC.
XX
XX      Mond JJ, Flora M, Kliman DM;
XX      WPI; 2002-130570/17.
XX
XX      New immunostimulatory compositions comprising RNA/DNA hybrid
XX      oligonucleotides, useful for enhancing an immune response or inducing
XX      cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX      HIV infection.
XX
XX      Example 11; Page 62; 68pp; English.
XX
XX      The present invention relates to an immunostimulatory composition, which
XX      comprises at least one oligonucleotide comprising both an RNA region and
XX      a DNA region. The composition is useful for enhancing an immune response
XX      or inducing cytokines. It can be used as a vaccine adjuvant and in
XX      treating diseases, including pathogenic infection, (non-)malignant
XX      tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX      colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX      (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX      hepatitis, HIV or malaria. The composition is also useful for treating,
XX      preventing or ameliorating the symptoms resulting from exposure to a bio-
XX      warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX      an immunostimulatory oligonucleotide described in the exemplification of
XX      the invention
XX
XX      Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
XX
XX      Query Match      100.0%; Score 20; DB 6; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 21;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1 GGTGACCGGTGCAGGGGGG 20
XX      |||||
XX      Db      1 GGTGACCGGTGCAGGGGGG 20
XX
XX      RESULT 4
XX      ABL35578
XX      ID ABL35578 standard; DNA; 20 BP.
XX
XX      AC      ABL35578;
XX
XX      DT      04-APR-2002 (first entry)
XX
XX      DE      Immunostimulatory oligonucleotide SEQ ID NO: 504.
XX
XX      DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX      infection; allergy; cancer; hypersensitivity; bio-warfare;
XX      immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX      immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX      antiinflammatory; antibacterial; ss.
XX
XX      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      misc_RNA      1..20
XX      /tag= a
XX      /note= "optionally thymidine is replaced by uracil to
FT      form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT      least one other base through a ribose sugar"
FT

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FT      form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT      least one other base through a ribose sugar"
XX
XX      WO200193902-A2.
XX
XX      13-DEC-2001.
XX
XX      07-JUN-2001; 2001WO-US018276.
XX
XX      07-JUN-2000; 2000US-0209797P.
XX
XX      (BIOS-) BIOSYNEXUS INC.
XX
XX      Mond JJ, Flora M, Kliman DM;
XX      WPI; 2002-130570/17.
XX
XX      New immunostimulatory compositions comprising RNA/DNA hybrid
XX      oligonucleotides, useful for enhancing an immune response or inducing
XX      cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX      HIV infection.
XX
XX      Example 11; Page 61; 68pp; English.
XX
XX      The present invention relates to an immunostimulatory composition, which
XX      comprises at least one oligonucleotide comprising both an RNA region and
XX      a DNA region. The composition is useful for enhancing an immune response
XX      or inducing cytokines. It can be used as a vaccine adjuvant and in
XX      treating diseases, including pathogenic infection, (non-)malignant
XX      tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX      colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX      (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX      hepatitis, HIV or malaria. The composition is also useful for treating,
XX      preventing or ameliorating the symptoms resulting from exposure to a bio-
XX      warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX      an immunostimulatory oligonucleotide described in the exemplification of
XX      the invention
XX
XX      Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
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XX      Query Match      100.0%; Score 20; DB 6; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 21;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1 GGTGACCGGTGCAGGGGGG 20
XX      |||||
XX      Db      1 GGTGACCGGTGCAGGGGGG 20
XX
XX      RESULT 5
XX      ABL35581
XX      ID ABL35581 standard; DNA; 20 BP.
XX
XX      AC      ABL35581;
XX
XX      DT      04-APR-2002 (first entry)
XX
XX      DE      Immunostimulatory oligonucleotide SEQ ID NO: 507.
XX
XX      DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX      infection; allergy; cancer; hypersensitivity; bio-warfare;
XX      immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX      immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX      antiinflammatory; antibacterial; ss.
XX
XX      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      misc_RNA      1..20
XX      /tag= a
XX      /note= "optionally thymidine is replaced by uracil to
FT      form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT      least one other base through a ribose sugar"
FT

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XX	PN	WO200193902-A2.
XX	PD	13-DEC-2001.
XX	PF	07-JUN-2001; 2001WO-US018276.
XX	PR	07-JUN-2001; 2001WO-US018276.
XX	PP	07-JUN-2001; 2001WO-US018276.
XX	PA	(BIOS-) BIOSYNEXUS INC.
XX	PI	Mond JJ, Flora M, Klinman DM;
XX	PI	WPI; 2002-130570/17.
XX	DR	New immunostimulatory compositions comprising RNA/DNA hybrid oligonucleotides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.
XX	PT	Example 11; Page 61; 68pp; English.
XX	PS	The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon, or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a bio-warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention
XX	CC	Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
XX	CC	Query Match 100.0%; Score 20; DB 6; Length 20;
XX	CC	Best Local Similarity 100.0%; Pred. No. 21;
XX	CC	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	QY	1 GGTGACCGGTGCAGGGGG 20
XX	DB	1 GGTGACCGGTGCAGGGGG 20
XX	RESULT 6	
XX	ABL35570	
XX	ID	ABL35570 standard; DNA; 20 BP.
XX	AC	ABL35570;
XX	DT	04-APR-2002 (first entry)
XX	DE	Immunostimulatory oligonucleotide SEQ ID NO: 496.
XX	KW	DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine; infection; allergy; cancer; hypersensitivity; bio-warfare;
XX	KW	immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX	KW	immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX	KW	antiinflammatory; antibacterial; ss.
XX	OS	Synthetic.
XX	Key	Location/Qualifiers
XX	misc_RNA	1. .20
XX	FT	/tag= a
XX	FT	/note= "optionally thymidine is replaced by uracil to form RNA or DNA/RNA hybrids. Thymidine is linked to at least one other base through a ribose sugar"
XX	PN	WO200193902-A2.
XX	PD	13-DEC-2001.

XX PF 07-JUN-2001; 2001WO-US018276.
 XX PR 07-JUN-2000; 2000US-0209797P.
 XX PA (BIOS-) BIOSYNEXUS INC.
 XX PI Mond JJ, Flora M, Klinman DM;
 XX DR WPI; 2002-130570/17.
 XX PT New immunostimulatory compositions comprising RNA/DNA hybrid
 PT oligonucleotides, useful for enhancing an immune response or inducing
 PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
 PT HIV infection.
 XX PS Example 11; Page 61; 68pp; English.
 XX CC The present invention relates to an immunostimulatory composition, which
 CC comprises at least one oligonucleotide comprising both an RNA region and
 CC a DNA region. The composition is useful for enhancing an immune response
 CC or inducing cytokines. It can be used as a vaccine adjuvant and in
 CC treating diseases, including pathogenic infection, (non-)malignant
 CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
 CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
 CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
 CC hepatitis, HIV or malaria. The composition is also useful for treating,
 CC preventing or ameliorating the symptoms resulting from exposure to a bio-
 CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
 CC an immunostimulatory oligonucleotide described in the exemplification of
 XX the invention
 XX SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGTGCACCGGTGCAGGGGG 20
 Db 1 GGTGCACCGGTGCAGGGGG 20
 RESULT 8
 ID ABK46470 standard; DNA; 20 BP.
 AC ABK46470;
 XX 05-JUN-2002 (first entry)
 DE Immunostimulatory unmethylated CpG oligodeoxynucleotide #60.
 XX unmethylated CpG; oligideoxynucleotide; ODN; virucide; vaccine;
 KW Paramyxoviridae; F protein; respiratory syncytial virus; RSV;
 KW viral bronchiolitis; pneumonia; infectious pulmonary disease;
 KW bronchopulmonary dysplasia; congenital heart condition; ss.
 XX Synthetic.
 OS WO200211761-A2.
 XX 14-FEB-2002.
 XX 09-AUG-2001; 2001WO-US041633.
 XX 10-AUG-2000; 2000US-0224011P.
 XX 01-SEP-2000; 2000US-0229307P.
 XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
 XX Mond JJ, Prince G, Klinman DM;
 XX

DR WPI; 2002-227118/28.
 XX Vaccine for immunizing patient against respiratory syncytial virus, has
 PT epitopes of Paramyxoviridae F protein, and cytosine followed by guanine
 PT linked by phosphate bond-oligodeoxynucleotides.
 XX Claim 4; Page 8; 30pp; English.
 XX CC The invention describes a vaccine comprising one or more epitopes of a
 CC Paramyxoviridae F protein, and one or more CpG (cytosine followed by
 CC guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The
 CC vaccine is useful for vaccinating a patient especially against viruses of
 CC the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the
 CC primary cause of viral bronchiolitis and pneumonia in infants and
 CC children, and infectious pulmonary disease in infants. RSV has been
 CC particularly implicated in death of infants that are premature, have
 CC bronchopulmonary dysplasia, or congenital heart conditions. This sequence
 CC represents an oligodeoxynucleotide that can be used in the creation of
 CC the vaccine
 XX SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGTGCACCGGTGCAGGGGG 20
 Db 1 GGTGCACCGGTGCAGGGGG 20
 RESULT 9
 ID ACC48296 standard; DNA; 20 BP.
 AC ACC48296;
 XX 11-AUG-2003 (first entry)
 DE CpG oligodeoxynucleotide D29 used for dendritic cell maturation.
 XX CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
 KW cytostatic; immunostimulant; gene therapy; ss.
 XX Synthetic.
 OS Key Location/Qualifiers
 PH modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate nucleotides"
 FT modified_base 1
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate nucleotide"
 XX WO2003020884-A2.
 XX 13-MAR-2003.
 XX 13-AUG-2002; 2002WO-US025732.
 XX 14-AUG-2001; 2001US-0312190P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Klinman DM, Gursel M, Verthelyi D;
 XX WPI; 2003-300874/29.
 XX Generating mature dendritic cells for tumor immunotherapy or as vaccines
 PT for activating the immune system to treat diseases such as cancer,
 PT comprises contacting a dendritic cell precursor with a D type

PT oligodeoxynucleotide.
 XX Claim 11; Page 44; 69pp; English.
 XX The present sequence is that of D type CpG oligodeoxynucleotide D29,
 CC which is used in a claimed method for generating a mature dendritic cell.
 CC The method involves contacting a dendritic cell precursor, especially a
 CC monocyte, with the oligonucleotide. The method is useful for generating
 CC mature dendritic cells and enhancing T cell responses, thus enhancing
 CC antigen presentation. Mature dendritic cells are useful for tumour
 CC immunotherapy, for augmenting an immune response to an infectious agent
 CC or to a vaccine, and as vaccines to prevent future infection or to
 CC activate the immune system to treat diseases such as cancer. Mature
 CC dendritic cells may also be used to produce activated T lymphocytes
 XX
 SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTGACCGGTGCAGGGGG 20
 Db 1 GGTGACCGGTGCAGGGGG 20
 RESULT 10
 ACC48313
 ID ACC48313 standard; DNA; 20 BP.
 AC ACC48313;
 XX
 DT 11-AUG-2003 (first entry)
 DE CpG oligodeoxynucleotide.
 XX
 KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
 KW cytostatic; immunostimulant; gene therapy; ss.
 XX Synthetic.
 OS
 XX WO2003020884-A2.
 XX
 PD 13-MAR-2003.
 XX
 PF 13-AUG-2002; 2002WO-US025732.
 XX
 PR 14-AUG-2001; 2001US-0312190P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Klinman DM, Gursel M, Verthelyi D;
 XX
 DR WPI; 2003-300874/29.
 XX
 PT Generating mature dendritic cells for tumor immunotherapy or as vaccines
 PT for activating the immune system to treat diseases such as cancer.
 PT comprises contacting a dendritic cell precursor with a D type
 PT oligodeoxynucleotide.
 XX
 PS Disclosure; Page 61; 69pp; English.
 XX
 CC The present sequence is that of a CpG oligodeoxynucleotide of the
 CC invention. A claimed method for generating dendritic cells involves
 CC contacting a dendritic cell precursor, especially a monocyte, with a D
 CC type oligodeoxynucleotide (see ACC48294) containing a central
 CC unmethylated CpG motif. The method is useful for generating mature
 CC dendritic cells and enhancing T cell responses, thus enhancing antigen
 CC presentation. Mature dendritic cells are useful for tumour immunotherapy,
 CC for augmenting an immune response to an infectious agent or to a vaccine,
 CC and as vaccines to prevent future infection or to activate the immune
 CC system to treat diseases such as cancer. Mature dendritic cells may also
 CC be used to produce activated T lymphocytes
 XX
 XX Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTGACCGGTGCAGGGGG 20
 Db 1 GGTGACCGGTGCAGGGGG 20
 RESULT 11
 ACC83118
 ID ACC83118 standard; DNA; 20 BP.
 AC ACC83118;
 XX
 DT 27-AUG-2003 (first entry)
 DE D class CpG ODN sequence useful for encapsulating in SSCL, DV29.
 XX
 KW Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
 KW tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
 KW thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
 KW schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
 KW asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
 KW CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
 KW multiple sclerosis; infection; tumour; ss.
 XX Unidentified.
 OS
 XX WO2003040308-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 29-JUL-2002; 2002WO-US024235.
 XX
 PR 27-JUL-2001; 2001US-0308283P.
 PR 25-JUL-2002; 2002US-00206407.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Klinman DM, Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK;
 XX
 DR WPI; 2003-482260/45.
 XX
 PT Cationic liposome composition for delivering oligodeoxynucleotides
 PT including a CpG motif in clinical applications, comprises a cationic
 PT lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
 XX
 PS Disclosure; Fig 10C; 110pp; English.
 XX
 CC The invention relates to sterically stabilised cationic liposomes (SSCL)
 CC which comprises a cationic lipid, a co-lipid, stabilising agent and
 CC encapsulating a k type oligodeoxynucleotide (ODN) including a CpG motif.
 CC The invention is useful in pharmaceutical composition for impairing
 CC growth of a solid tumour cell (e.g. human tumour cell) bearing an
 CC interleukin-13 receptor in a subject; for stimulating an immune response,
 CC which is expression of a cytokine (e.g. interferon gamma), particularly
 CC immunotherapeutic response against tumours or stimulating an in vivo or
 CC an in vitro immune cell, and for inducing an immune response against an
 CC infectious agent e.g. virus, bacteria and fungus. It is also useful for
 CC delivering oligodeoxynucleotides including a CpG motif in clinical
 CC applications; for treating infectious diseases (e.g. tularemia, malaria,
 CC francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
 CC (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer
 CC etc), allergy (e.g. eczema, allergic rhinitis or coryza), hay fever,
 CC bronchial or allergic asthma, urticaria, food allergies, autoimmune
 CC diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and
 CC multiple sclerosis) and psoriasis. The present sequence is a D class CpG
 CC ODN potentially useful for encapsulating in SSCL
 XX

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SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGACCGGTGCAGGGGG 20
Db 1 GGTGACCGGTGCAGGGGG 20

RESULT 12
ACC83152
ID ACC83152 standard; DNA; 20 BP.
XX ACC83152;
AC ACC83152;
DT 27-AUG-2003 (first entry)
DE D class ODN sequence useful for encapsulating in SSCL, D29.
KW Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
KW tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
KW thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
KW schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
KW asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
KW CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
KW multiple sclerosis; infection; tumour; phosphorothioate backbone; ss.
XX Unidentified.
XX Key Location/Qualifiers
FH modified_base 16..20
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "Phosphorothioate backbone"
XX WO2003040308-A2.
XX 15-MAY-2003.
XX 29-JUL-2002; 2002WO-US024235.
XX 27-JUL-2001; 2001US-0308283P.
XX 25-JUL-2002; 2002US-00206407.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Klinman DM, Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK;
XX WPI; 2003-482260/45.
XX Cationic liposome composition for delivering oligodeoxynucleotides
XX including a CpG motif in clinical applications, comprises a cationic
XX lipid, a co-lipid, stabilising agent and an encapsulated oligonucleotide.
XX Example 8; Page 52; 110pp; English.
XX The invention relates to sterically stabilised cationic liposomes (SSCL)
XX which comprises a cationic lipid, a co-lipid, stabilising agent and
XX encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.
XX The invention is useful in pharmaceutical composition for impairing
XX growth of a solid tumour cell (e.g. human tumour cell) bearing an
XX interleukin-13 receptor in a subject; for stimulating an immune response,
XX which is expression of a cytokine (e.g. interferon gamma), particularly
XX immunotherapeutic response against tumours or stimulating an in vivo or
XX an in vitro immune cell, and for inducing an immune response against an
XX infectious agent e.g. virus, bacteria and fungus. It is also useful for
XX delivering oligodeoxynucleotides including a CpG motif in clinical
XX applications; for treating infectious diseases (e.g. tularemia, malaria,
XX francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
XX (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer
XX etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,
CC bronchial or allergic asthma, urticaria, food allergies), autoimmune
CC diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and
CC multiple sclerosis) and psoriasis. The present sequence is a D class ODN
CC potentially useful for encapsulating in SSCL
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGACCGGTGCAGGGGG 20
Db 1 GGTGACCGGTGCAGGGGG 20

RESULT 13
ADD01049
ID ADD01049 standard; DNA; 20 BP.
XX ADD01049;
AC ADD01049;
DT 01-JAN-2004 (first entry)
DE CpG D oligonucleotide SEQ ID NO:13.
KW vascular endothelial growth factor; VEGF; CpG oligonucleotide;
KW neovascularisation; angiogenesis; vulnery; vasotropic;
KW antiarteriosclerotic; gene therapy; skin graft; male pattern baldness;
KW atherosclerosis; ischaemia; ss.
XX Synthetic.
XX WO2003054161-A2.
XX 03-JUL-2003.
XX 19-DEC-2002; 2002WO-US040955.
XX 20-DEC-2001; 2001US-0343457P.
XX (UYTE-) UNIV TENNESSEE RES CORP.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Klinman DM, Zheng M, Rouse BT;
XX WPI; 2003-559139/52.
XX Inducing the production of vascular endothelial growth factor by a cell,
XX useful for inducing angiogenesis, comprises contacting the cell with a
XX CpG oligodeoxynucleotide.
XX Example 7; SEQ ID NO 13; 37pp; English.
XX The present invention describes a method for inducing the production of
XX vascular endothelial growth factor (VEGF) by a cell comprising contacting
XX the cell with a CpG oligonucleotide and therefore inducing the production
XX of VEGF by the cell. Also described: (1) inducing neovascularisation in a
XX tissue, comprising introducing a CpG oligonucleotide into an area of the
XX tissue where the formation of new blood vessels is desired, and so
XX inducing neovascularisation in the area of the tissue; (2) promoting
XX angiogenesis in an area of the subject where angiogenesis is desired,
XX comprising introducing a CpG oligonucleotide to the area, and so
XX promoting angiogenesis in the subject; and (3) screening for an agent
XX that inhibits neovascularisation, comprising administering a CpG
XX oligonucleotide to a non-human mammal and administering the agent to the
XX mammal, where inhibition of angiogenesis in the animal indicates that the
XX agent is effective in inhibiting neovascularisation. The CpG
XX oligonucleotides have vulnery, vasotropic and antiarteriosclerotic
XX activities, and can be used in gene therapy. The method and the CpG
XX oligonucleotides can be used in inducing angiogenesis or
XX neovascularisation, such as in subjects with a skin graft, subjects who
XX exhibit male pattern baldness, or subjects who have a wound or who have
```

CC atherosclerosis or ischaemia. The method may also be used in screening
 CC for agents that inhibit neovascularisation. The present sequence
 CC represents a CpG oligonucleotide which is used in the exemplification of
 CC the present invention.

XX
 SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 |||||
 Db 1 GGTGCACCGGTGCAGGGGG 20

RESULT 14
 ABL35599
 ID ABL35599 standard; DNA; 28 BP.

XX ABL35599;

XX 04-APR-2002 (first entry)

XX Immunostimulatory oligonucleotide SEQ ID NO: 525.

XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
 XX infection; allergy; cancer; hypersensitivity; bio-warfare;
 KW immunostimulant; anti-allergic; cytostatic; antimicrobial; anti-HIV;
 KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
 XX anti-inflammatory; antibacterial; ss.

XX Synthetic.

XX Key Location/Qualifiers
 FH misc_RNA 1..28
 FT /tag= a

FT /note= "optionally thymidine is replaced by uracil to
 FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
 FT least one other base through a ribose sugar"

XX WO200193902-A2.

XX 13-DEC-2001.

XX 07-JUN-2001; 2001WO-US018276.

XX 07-JUN-2000; 2000US-0209797P.

XX (BIOS-) BIOSYNEXUS INC.

XX Mond JJ, Flora M, Klinman DM;

XX WPI; 2002-130570/17.

XX New immunostimulatory compositions comprising RNA/DNA hybrid
 PT oligonucleotides, useful for enhancing an immune response or inducing
 PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
 PT HIV infection.

XX Example 11; Page 61; 68pp; English.

XX The present invention relates to an immunostimulatory composition, which
 XX comprises at least one oligonucleotide comprising both an RNA region and
 CC a DNA region. The composition is useful for enhancing an immune response
 CC or inducing cytokines. It can be used as a vaccine adjuvant and in
 CC treating diseases, including pathogenic infection, (non-)malignant
 CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
 CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
 CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
 CC hepatitis, HIV or malaria. The composition is also useful for treating,
 CC preventing or ameliorating the symptoms resulting from exposure to a bio-
 CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is

CC an immunostimulatory oligonucleotide described in the exemplification of
 CC the invention

XX Sequence 28 BP; 10 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

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 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
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 Db 1 GGTGCACCGGTGCAGGGGG 20

RESULT 15
 ABL35603
 ID ABL35603 standard; DNA; 28 BP.

XX ABL35603;

XX 04-APR-2002 (first entry)

XX Immunostimulatory oligonucleotide SEQ ID NO: 529.

XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
 KW infection; allergy; cancer; hypersensitivity; bio-warfare;
 KW immunostimulant; anti-allergic; cytostatic; antimicrobial; anti-HIV;
 KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
 XX anti-inflammatory; antibacterial; ss.

XX Synthetic.

XX Key Location/Qualifiers
 FH misc_RNA 1..28
 FT /tag= a

FT /note= "optionally thymidine is replaced by uracil to
 FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
 FT least one other base through a ribose sugar"

XX WO200193902-A2.

XX 13-DEC-2001.

XX 07-JUN-2001; 2001WO-US018276.

XX 07-JUN-2000; 2000US-0209797P.

XX (BIOS-) BIOSYNEXUS INC.

XX Mond JJ, Flora M, Klinman DM;

XX WPI; 2002-130570/17.

XX New immunostimulatory compositions comprising RNA/DNA hybrid
 PT oligonucleotides, useful for enhancing an immune response or inducing
 PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
 PT HIV infection.

XX Example 11; Page 61; 68pp; English.

XX The present invention relates to an immunostimulatory composition, which
 CC comprises at least one oligonucleotide comprising both an RNA region and
 CC a DNA region. The composition is useful for enhancing an immune response
 CC or inducing cytokines. It can be used as a vaccine adjuvant and in
 CC treating diseases, including pathogenic infection, (non-)malignant
 CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
 CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
 CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
 CC hepatitis, HIV or malaria. The composition is also useful for treating,
 CC preventing or ameliorating the symptoms resulting from exposure to a bio-
 CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
 CC an immunostimulatory oligonucleotide described in the exemplification of
 CC the invention

XX
SQ Sequence 28 BP; 4 A; 6 C; 13 G; 5 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGTGCACCGGTGCAGGGGG 20
Db 9 GGTGCACCGGTGCAGGGGG 28

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SUMMARIES

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C 3	15.8	79.0	3358	3	US-09-248-571-2
C 4	15.8	79.0	3358	4	US-09-553-736-2
C 5	15.8	79.0	10827	1	US-08-060-925A-12
C 6	15.8	79.0	12222	4	US-09-328-925-42
C 7	15.4	77.0	366	4	US-09-489-039A-5836
C 8	15.2	76.0	480	4	US-09-252-991A-5639
C 9	15.2	76.0	564	4	US-09-252-991A-5555
C 10	15.2	76.0	774	4	US-09-252-991A-5590
C 11	15.2	76.0	1083	4	US-09-655-270A-20
C 12	15.2	76.0	1098	4	US-09-651-941-24
C 13	15.2	76.0	1098	4	US-09-955-597-24
C 14	15.2	76.0	12508	4	US-09-655-270A-1
C 15	15.2	76.0	12523	4	US-09-651-941-1
C 16	15.2	76.0	12523	4	US-09-955-597-1
C 17	15.2	76.0	24707	4	US-09-740-027-3
C 18	15.2	76.0	45546	4	US-09-146-053-6
C 19	15.2	76.0	4403765	3	US-09-103-840A-2
C 20	15.2	76.0	4411529	3	US-09-103-840A-1
C 21	14.8	74.0	1443	3	US-08-959-381A-3
C 22	14.8	74.0	1446	4	US-09-170-496D-81
C 23	14.8	74.0	1446	4	US-09-170-496D-207
C 24	14.8	74.0	1626	3	US-08-959-381A-4
C 25	14.8	74.0	4000	2	US-08-687-289A-2
C 26	14.8	74.0	4000	4	US-09-435-897-2
C 27	14.8	74.0	4300	1	US-08-041-538-1

C 28	14.8	74.0	4300	1	US-08-463-642-1
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C 30	14.8	74.0	4300	2	US-08-465-157-1
C 31	14.8	74.0	4300	5	PCT-US91-09422-1
C 32	14.8	74.0	5236	5	PCT-US91-09422-16
C 33	14.8	74.0	6836	4	US-08-976-259-73
C 34	14.4	72.0	265	4	US-09-313-294A-385
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C 36	14.4	72.0	2194	4	US-09-023-655-668
C 37	14.4	72.0	2511	3	US-03-422-869-19
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C 39	14.2	71.0	96	4	US-09-342-681C-107
C 40	14.2	71.0	236	4	US-09-621-976-18710
C 41	14.2	71.0	339	4	US-09-016-434-714
C 42	14.2	71.0	419	4	US-09-833-381-1374
C 43	14.2	71.0	548	1	US-08-459-667-6
C 44	14.2	71.0	548	4	US-09-224-110-6
C 45	14.2	71.0	548	5	PCT-US95-07289-6

ALIGNMENTS

RESULT 1
US-09-922-445-1/c
; Sequence 1, Application US/09922445
; Patent No. 6528268
; GENERAL INFORMATION:
; APPLICANT: Andersson, Maria K.
; APPLICANT: Berglund, Lars G. T.
; APPLICANT: Reneland, Rikard H.
; APPLICANT: Adam, Gail I. R.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
; FILE REFERENCE: G6126US
; CURRENT APPLICATION NUMBER: US/09/922,445
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 38653
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(26156)
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; NAME/KEY: misc feature
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; OTHER INFORMATION: nucleotide 24801 is a single nucleotide polymorphism which can
; OTHER INFORMATION: A or G
; NAME/KEY: misc feature
; LOCATION: (24941)..(24941)
; OTHER INFORMATION: nucleotide 24941 is a single nucleotide polymorphism which can
; OTHER INFORMATION: T or C
; NAME/KEY: exon
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; NAME/KEY: Intron
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; NAME/KEY: exon
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; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (27025)..(27178)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (27179)..(30519)
; OTHER INFORMATION:
; NAME/KEY: misc feature

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; LOCATION: (27645)..(27645)
; OTHER INFORMATION: nucleotide 27645 is a single nucleotide polymorphism which can be
; OTHER INFORMATION: C or G
; NAME/KEY: exon
; LOCATION: (30520)..(30681)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (30682)..(30894)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (30895)..(31027)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (31028)..(31747)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (31748)..(31841)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (31842)..(32400)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (32163)..(32163)
; OTHER INFORMATION: nucleotide 32163 is a single nucleotide polymorphism which can be
; OTHER INFORMATION: A or C
; NAME/KEY: exon
; LOCATION: (32401)..(32528)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (32529)..(33414)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (32614)..(32614)
; OTHER INFORMATION: nucleotide 32614 is a single nucleotide polymorphism which can be
; OTHER INFORMATION: A or G
; NAME/KEY: exon
; LOCATION: (33415)..(33597)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (33598)..(34314)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (34315)..(34588)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (34589)..(36404)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (36405)..(36523)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (36524)..(38341)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (38342)..(38653)
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank/AC004923
; DATABASE ENTRY DATE: 1999-12-21
; RELEVANT RESIDUES: (1)..(38653)
US-09-922-445-1

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Query Match      84.0%; Score 16.8; DB 4; Length 38653;
Best Local Similarity 90.0%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 GGTGCACCGGTGCAGGGGG 20
Db 14714 GGTGCACTGGGCGAGGGGG 14695

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RESULT 2
US-09-489-039A-2752

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; Sequence 2752, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 2752
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2752

```

```

Query Match      79.0%; Score 15.8; DB 4; Length 633;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 GGTGCACCGGTGCAGGGGG 19
Db 614 GGTGCACCGGTGCAGGGGG 632

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RESULT 3
US-09-248-571-2
; Sequence 2, Application US/09248571
; Patent No. 6136539
; GENERAL INFORMATION:
; APPLICANT: BASBAUM, CAROL
; APPLICANT: GALLUP, MARIANNE
; APPLICANT: DAIZONG, LI
; APPLICANT: GEBREMICHAEL, ASSEFA
; APPLICANT: GENSGH, ERIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITION OF MUC-5 MUCIN
; FILE REFERENCE: UCSF12/02
; CURRENT APPLICATION NUMBER: US/09/248,571
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: 60/074,398
; EARLIER FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3358
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-248-571-2

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Query Match      79.0%; Score 15.8; DB 3; Length 3358;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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```

Qy 2 GTGCACCGGTGCAGGGGG 20
Db 998 GTGCACCGGTGCAGGGGG 1016

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```

RESULT 4
US-09-553-736-2
; Sequence 2, Application US/09553736
; Patent No. 6440672
; GENERAL INFORMATION:
; APPLICANT: BASBAUM, CAROL
; APPLICANT: GALLUP, MARIANNE
; APPLICANT: DAIZONG, LI
; APPLICANT: GEBREMICHAEL, ASSEFA
; APPLICANT: GENSGH, ERIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE INHIBITION OF MUC-5
; MUCIN GENE EXPRESSION

```


FILE REFERENCE: UCSF-012/03US
CURRENT APPLICATION NUMBER: US/09/553,736
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US/09/248,571
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: US/09/074,398
PRIOR FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 3358
TYPE: DNA
ORGANISM: Homo sapiens
US-09-553-736-2

Query Match 79.0%; Score 15.8; DB 4; Length 3358;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTGCACCGGTGACGGGGG 20
Db 998 GTGCACCGGTGACGGGGG 1016

RESULT 5
US-08-060-925A-12
Sequence 12, Application US/08060925A
Patent No. 5439824
GENERAL INFORMATION:

APPLICANT: Brantley, Mark
APPLICANT: Laubach, Victor
TITLE OF INVENTION: INCREASED EXPRESSION OF ALPHA-1
TITLE OF INVENTION: ANTI-TRYPsin IN EXPRESSION VECTORS THROUGH THE INCLUSION OF
TITLE OF INVENTION: INTRON II
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: KNOBBE, MARTENS, OLSON AND BEAR
STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
CITY: NEWPORT BEACH
STATE: CA
COUNTRY: USA
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/060,925A
FILING DATE: 06-MAY-1993

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael L.
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH040.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 10627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-060-925A-12

Query Match 79.0%; Score 15.8; DB 1; Length 10627;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTCACCGGTGACGGGGG 19
Db 10086 GGTCACCGGTGACGGGGG 10104

RESULT 6
US-09-328-925-42
Sequence 42, Application US/09328925
Patent No. 5610906
GENERAL INFORMATION:
APPLICANT: Kurachi, Kotoku
APPLICANT: Kurachi, Sumiko
TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: US-03603
CURRENT APPLICATION NUMBER: US/09/328,925
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 42
LENGTH: 12222
TYPE: DNA
ORGANISM: Homo sapiens
US-09-328-925-42

Query Match 79.0%; Score 15.8; DB 4; Length 12222;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTCACCGGTGACGGGGG 19
Db 11680 GGTCACCGGTGACGGGGG 11698

RESULT 7
US-09-489-039A-5836
Sequence 5836, Application US/09489039A
Patent No. 5610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US/09/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 5836
LENGTH: 366
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5836

Query Match 77.0%; Score 15.4; DB 4; Length 366;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTCACCGGTGACGGG 17
Db 70 GGTCACCGGTGACGGG 86

RESULT 8
US-09-252-991A-5639
Sequence 5639, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5639
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5639

Query Match 76.0%; Score 15.2; DB 4; Length 480;
Best Local Similarity 85.0%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
|||||
DB 391 GGTGCGCGGTGCAGTGGAG 410

RESULT 9

US-09-252-991A-5555/c
; Sequence 5555, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09252991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5555
; LENGTH: 564
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5555

Query Match 76.0%; Score 15.2; DB 4; Length 564;
Best Local Similarity 85.0%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
|||||
DB 181 GGTGCGCGGTGCAGTGGAG 162

RESULT 10

US-09-252-991A-5590/c
; Sequence 5590, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09252991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5590
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5590

Query Match 76.0%; Score 15.2; DB 4; Length 774;
Best Local Similarity 85.0%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
|||||
DB 363 GGTGCGCGGTGCAGTGGAG 344

RESULT 11

US-09-655-270A-20
; Sequence 20, Application US/09655270A
; Patent No. 6329151
; GENERAL INFORMATION:
; APPLICANT: Rouviere, Pierre E.
; TITLE OF INVENTION: High Density Sampling of Differentially Expressed Prokaryotic
; FILE REFERENCE: BC1011 US NA
; CURRENT APPLICATION NUMBER: US/09/655,270A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/120,702
; PRIOR FILING DATE: 1999-February-19
; PRIOR APPLICATION NUMBER: 60/152,542
; PRIOR FILING DATE: 1999-September-03
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 1083
; TYPE: DNA
; ORGANISM: Rhodococcus erythropolis HL PM-1
US-09-655-270A-20

Query Match 76.0%; Score 15.2; DB 4; Length 1083;
Best Local Similarity 85.0%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
|||||
DB 334 GGTGCACCGGTGCTGGCGG 353

RESULT 12

US-09-651-941-24
; Sequence 24, Application US/09651941
; Patent No. 6355470
; GENERAL INFORMATION:
; APPLICANT: ROUVIER, PIERRE E
; APPLICANT: WALTERS, DANA M
; APPLICANT: RAINER, RUSS
; TITLE OF INVENTION: Genes Encoding Picric Acid Degradation
; FILE REFERENCE: BC1022 US NA
; CURRENT APPLICATION NUMBER: US/09/651,941
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,545
; PRIOR FILING DATE: 1999-10-03
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Rhodococcus erythropolis HL PM-1
US-09-651-941-24

Query Match 76.0%; Score 15.2; DB 4; Length 1098;
Best Local Similarity 85.0%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
|||||
DB 334 GGTGCACCGGTGCTGGCGG 353

RESULT 13

US-09-955-597-24
 ; Sequence 24, Application US/09955597
 ; Patent No. 6461856
 ; GENERAL INFORMATION:
 ; APPLICANT: ROUVIER, PIERRE E
 ; APPLICANT: WALTERS, DANA M
 ; APPLICANT: RAINIER, RUSS
 ; TITLE OF INVENTION: Genes Encoding Picric Acid Degradation
 ; FILE REFERENCE: BC1022 US NA
 ; CURRENT APPLICATION NUMBER: US/09/955,597
 ; CURRENT FILING DATE: 2001-09-17
 ; PRIOR APPLICATION NUMBER: 60/152,545
 ; PRIOR FILING DATE: 1999-10-03
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 24
 ; LENGTH: 1698
 ; TYPE: DNA
 ; ORGANISM: Rhodococcus erythropolis HL PM-1
 US-09-955-597-24

Query Match 76.0%; Score 15.2; DB 4; Length 1098;
 Best Local Similarity 85.0%; Pred. No. 3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GGTGACCGGTGTCAGGGGG 20
 |||||
 Db 334 GGTGACCGGTGTCAGGGGG 353

RESULT 14
 US-09-655-270A-1
 ; Sequence 1, Application US/09655270A
 ; Patent No. 6329151
 ; GENERAL INFORMATION:
 ; APPLICANT: Rouviere, Pierre E.
 ; TITLE OF INVENTION: High Density Sampling of Differentially Expressed Prokaryotic m
 ; FILE REFERENCE: BC1011 US NA
 ; CURRENT APPLICATION NUMBER: US/09/655,270A
 ; CURRENT FILING DATE: 2000-09-05
 ; PRIOR APPLICATION NUMBER: 60/120,702
 ; PRIOR FILING DATE: 1999-February-19
 ; PRIOR APPLICATION NUMBER: 60/152,542
 ; PRIOR FILING DATE: 1999-September-03
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 1
 ; LENGTH: 12508
 ; TYPE: DNA
 ; ORGANISM: Rhodococcus erythropolis HL PM-1
 US-09-655-270A-1

Query Match 76.0%; Score 15.2; DB 4; Length 12508;
 Best Local Similarity 85.0%; Pred. No. 2.9e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GGTGACCGGTGTCAGGGGG 20
 |||||
 Db 11759 GGTGACCGGTGTCAGGGGG 11778

RESULT 15
 US-09-651-941-1
 ; Sequence 1, Application US/09651941
 ; Patent No. 6355470
 ; GENERAL INFORMATION:
 ; APPLICANT: ROUVIER, PIERRE E
 ; APPLICANT: WALTERS, DANA M
 ; APPLICANT: RAINIER, RUSS
 ; TITLE OF INVENTION: Genes Encoding Picric Acid Degradation
 ; FILE REFERENCE: BC1022 US NA
 ; CURRENT APPLICATION NUMBER: US/09/651,941
 ; CURRENT FILING DATE: 2000-08-31

; PRIOR APPLICATION NUMBER: 60/152,545
 ; PRIOR FILING DATE: 1999-10-03
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 1
 ; LENGTH: 12523
 ; TYPE: DNA
 ; ORGANISM: Rhodococcus erythropolis HL PM-1
 US-09-651-941-1
 Query Match 76.0%; Score 15.2; DB 4; Length 12523;
 Best Local Similarity 85.0%; Pred. No. 2.9e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GGTGACCGGTGTCAGGGGG 20
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 Db 11759 GGTGACCGGTGTCAGGGGG 11778
 Search completed: July 2, 2004, 13:37:22
 Job time : 36.3415 secs

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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:11:05 ; Search time 154.146 Seconds
(without alignments)
625.926 Million cell updates/sec

Title: US-10-068-160-2

Perfect score: 20
Sequence: 1 ggtgcaccggtgcaggggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA.*
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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	13	US-09-874-991C-496
2	20	100.0	20	13	US-09-874-991C-504
3	20	100.0	20	13	US-09-874-991C-507
4	20	100.0	20	13	US-09-874-991C-514
5	20	100.0	20	13	US-09-874-991C-540
6	20	100.0	20	15	US-10-068-160-2
7	20	100.0	20	15	US-10-194-035-42
8	20	100.0	20	17	US-10-666-022-178
9	20	100.0	28	13	US-09-874-991C-517
10	20	100.0	28	13	US-09-874-991C-525
11	20	100.0	28	13	US-09-874-991C-529
12	20	100.0	28	13	US-09-874-991C-537
13	20	100.0	40	13	US-09-874-991C-548
14	18.4	92.0	20	13	US-09-874-991C-495

Sequence 499, App
Sequence 506, App
Sequence 510, App
Sequence 543, App
Sequence 37, Appl
Sequence 58, Appl
Sequence 101, App
Sequence 516, App
Sequence 526, App
Sequence 528, App
Sequence 532, App
Sequence 13, Appl
Sequence 2, Appl
Sequence 22, Appl
Sequence 454, App
Sequence 505, App
Sequence 538, App
Sequence 1, Appl
Sequence 5, Appl
Sequence 30, Appl
Sequence 41, Appl
Sequence 54, Appl
Sequence 60, Appl
Sequence 61, Appl
Sequence 63, Appl
Sequence 32, Appl
Sequence 34, Appl
Sequence 37, Appl
Sequence 38, Appl
Sequence 43, Appl
Sequence 72, Appl

ALIGNMENTS

RESULT 1

US-09-874-991C-496
; Sequence 496, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 496
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-496

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGTGCAGGGGG 20
DB 1 GGTGCACCGTGCAGGGGG 20

RESULT 2

US-09-874-991C-504
; Sequence 504, Application US/09874991C
; Publication No. US20040052763A1

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/ GENERAL INFORMATION:
/ APPLICANT: MOND, JAMES J.
/ APPLICANT: FLORA, MICHAEL
/ APPLICANT: KLINMAN, DENNIS M.
/ TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
/ CURRENT APPLICATION NUMBER: US/09/874,991C
/ CURRENT FILING DATE: 2001-06-07
/ PRIOR APPLICATION NUMBER: 60/209,797
/ PRIOR FILING DATE: 2000-06-07
/ NUMBER OF SEQ ID NOS: 620
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 504
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-504

Query Match          100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 20
Db 1 GGTGCACCGGTGCAGGGGG 20

RESULT 3
US-09-874-991C-507
/ Sequence 507, Application US/09874991C
/ Publication No. US20040052763A1
/ GENERAL INFORMATION:
/ APPLICANT: MOND, JAMES J.
/ APPLICANT: FLORA, MICHAEL
/ APPLICANT: KLINMAN, DENNIS M.
/ TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
/ FILE REFERENCE: 07787.0042-0
/ CURRENT APPLICATION NUMBER: US/09/874,991C
/ CURRENT FILING DATE: 2001-06-07
/ PRIOR APPLICATION NUMBER: 60/209,797
/ PRIOR FILING DATE: 2000-06-07
/ NUMBER OF SEQ ID NOS: 620
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 507
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-507

Query Match          100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 20
Db 1 GGTGCACCGGTGCAGGGGG 20

RESULT 4
US-09-874-991C-514
/ Sequence 514, Application US/09874991C
/ Publication No. US20040052763A1
/ GENERAL INFORMATION:
/ APPLICANT: MOND, JAMES J.
/ APPLICANT: FLORA, MICHAEL
/ APPLICANT: KLINMAN, DENNIS M.
/ TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
/ FILE REFERENCE: 07787.0042-0
/ CURRENT APPLICATION NUMBER: US/09/874,991C
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/ CURRENT FILING DATE: 2001-06-07
/ PRIOR APPLICATION NUMBER: 60/209,797
/ PRIOR FILING DATE: 2000-06-07
/ NUMBER OF SEQ ID NOS: 620
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 514
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-514

Query Match          100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 20
Db 1 GGTGCACCGGTGCAGGGGG 20

RESULT 5
US-09-874-991C-540
/ Sequence 540, Application US/09874991C
/ Publication No. US20040052763A1
/ GENERAL INFORMATION:
/ APPLICANT: MOND, JAMES J.
/ APPLICANT: FLORA, MICHAEL
/ APPLICANT: KLINMAN, DENNIS M.
/ TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
/ FILE REFERENCE: 07787.0042-0
/ CURRENT APPLICATION NUMBER: US/09/874,991C
/ CURRENT FILING DATE: 2001-06-07
/ PRIOR APPLICATION NUMBER: 60/209,797
/ PRIOR FILING DATE: 2000-06-07
/ NUMBER OF SEQ ID NOS: 620
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 540
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-540

Query Match          100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 20
Db 1 GGTGCACCGGTGCAGGGGG 20

RESULT 6
US-10-068-160-2
/ Sequence 2, Application US/10068160
/ Publication No. US200306040A1
/ GENERAL INFORMATION:
/ APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
/ APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
/ APPLICANT: KLINMAN, DENNIS
/ APPLICANT: ISHII, Ken
/ APPLICANT: VERTHELYI, Daniela
/ TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
/ FILE REFERENCE: 4239-61999
/ CURRENT APPLICATION NUMBER: US/10/068,160
/ CURRENT FILING DATE: 2002-02-06
/ PRIOR APPLICATION NUMBER: 60/128,898
/ PRIOR FILING DATE: 1999-04-12
/ NUMBER OF SEQ ID NOS: 120
/ SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-2

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGACCGGTGCAGGGGG 20
|||
Db 1 GGTGACCGGTGCAGGGGG 20

RESULT 7

US-10-194-035-42
; Sequence 42, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLIMAN, DENNIS
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-42

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGACCGGTGCAGGGGG 20
|||
Db 1 GGTGACCGGTGCAGGGGG 20

RESULT 8

US-10-666-022-178
; Sequence 178, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Kliman, Dennis M.
; APPLICANT: Verchelyi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 178

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-666-022-178

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGACCGGTGCAGGGGG 20
|||
Db 1 GGTGACCGGTGCAGGGGG 20

RESULT 9

US-09-874-991C-517
; Sequence 517, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 517
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-517

Query Match 100.0%; Score 20; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGACCGGTGCAGGGGG 20
|||
Db 1 GGTGACCGGTGCAGGGGG 20

RESULT 10

US-09-874-991C-525
; Sequence 525, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 525
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-525

Query Match 100.0%; Score 20; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
DB 1 GGTGCACCGGTGCAGGGGG 20

RESULT 11

US-09-874-991C-529
; Sequence 529, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 529
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR

US-09-874-991C-529
Query Match 100.0%; Score 20; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
DB 9 GGTGCACCGGTGCAGGGGG 28

RESULT 12

US-09-874-991C-537
; Sequence 537, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 537
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR

US-09-874-991C-537
Query Match 100.0%; Score 20; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
DB 9 GGTGCACCGGTGCAGGGGG 28

Query Match 100.0%; Score 20; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
DB 1 GGTGCACCGGTGCAGGGGG 20

RESULT 13

US-09-874-991C-548
; Sequence 548, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 548
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR

US-09-874-991C-548
Query Match 100.0%; Score 20; DB 13; Length 40;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
DB 14 GGTGCACCGGTGCAGGGGG 33

RESULT 14

US-09-874-991C-495
; Sequence 495, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 495
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR

US-09-874-991C-495
Query Match 92.0%; Score 18.4; DB 13; Length 20;
Best Local Similarity 95.0%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
DB 1 GGTGCACCGGTGCAGGGGG 20

RESULT 15

US-09-874-991C-499
; Sequence 499, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:

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; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 499
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-499

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Query Match      92.0%; Score 18.4; DB 13; Length 20;
Best Local Similarity 95.0%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 GGTGCACCGGTGCAGGGGG 20
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Db      1 GGTGCACCGGTGCAGGGGG 20

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Search completed: July 2, 2004, 13:58:23
Job time : 154.146 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:38:45 ; Search time 1497.8 Seconds

(without alignments)
398.746 Million cell updates/sec

Title: US-10-068-160-2

Perfect score: 20

Sequence: 1 ggtgaccggtgcaggggg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

- 1: em_estbta.*
- 2: em_esthum.*
- 3: em_estin.*
- 4: em_estm.*
- 5: em_estov.*
- 6: em_estpi.*
- 7: em_estro.*
- 8: em_hrc.*
- 9: gb_est1.*
- 10: gb_est2.*
- 11: gb_hrc.*
- 12: gb_est3.*
- 13: gb_est4.*
- 14: gb_est5.*
- 15: em_estfun.*
- 16: em_estom.*
- 17: em_gss_hum.*
- 18: em_gss_inv.*
- 19: em_gss_pln.*
- 20: em_gss_vrt.*
- 21: em_gss_fun.*
- 22: em_gss_fam.*
- 23: em_gss_mus.*
- 24: em_gss_pro.*
- 25: em_gss_rod.*
- 26: em_gss_phg.*
- 27: em_gss_vri.*
- 28: gb_gss1.*
- 29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	18.4	92.0	339	14	CB076094
c 2	18.4	92.0	440	14	CB087231
c 3	18.4	92.0	509	14	CB087214
c 4	18.4	92.0	598	14	CB087525

5	18.4	92.0	340	29	CG271799
6	17.4	87.0	610	29	CG692380
7	17.4	87.0	779	28	CC109078
8	17.4	87.0	799	28	CC133230
9	17.4	87.0	1005	29	CNS04021
10	17.4	87.0	1200	13	EX426076
11	17.4	87.0	1214	13	BO898390
12	17.4	85.0	354	9	AV393217
13	16.8	84.0	432	10	BE388878
14	16.8	84.0	237	28	AZ492326
15	16.8	84.0	275	10	BB496626
16	16.8	84.0	289	9	AV219401
17	16.8	84.0	293	13	BY103614
18	16.8	84.0	323	9	AL898002
19	16.8	84.0	383	28	BZ782509
20	16.8	84.0	402	29	CE182406
21	16.8	84.0	421	9	AL897989
22	16.8	84.0	430	28	BZ422920
23	16.8	84.0	513	29	CE284352
24	16.8	84.0	562	9	AI370313
25	16.8	84.0	615	12	BJ252893
26	16.8	84.0	618	10	BE973745
27	16.8	84.0	619	14	CD771763
28	16.8	84.0	630	28	BZ335826
29	16.8	84.0	631	12	BJ244833
30	16.8	84.0	646	13	CA100132
31	16.8	84.0	646	29	CB419868
32	16.8	84.0	671	12	BJ229325
33	16.8	84.0	677	28	BE886902
34	16.8	84.0	684	12	BE624520
35	16.8	84.0	685	12	BE634520
36	16.8	84.0	692	12	BE620160
37	16.8	84.0	697	12	BJ250701
38	16.8	84.0	708	12	BE621890
39	16.8	84.0	740	12	BE617983
40	16.8	84.0	748	28	BZ863203
41	16.8	84.0	768	12	BE674536
42	16.8	84.0	769	14	CF765888
43	16.8	84.0	782	10	BF582545
44	16.8	84.0	811	29	CNS041X0
45	16.8	84.0	815	12	BI334719

ALIGNMENTS

RESULT 1	CB076094/c
LOCUS	339 bp mRNA linear EST 24-JAN-2003
DEFINITION	h37c06.g1 Hedyotis terminalis flower - Stage 2 (NYBG) Hedyotis terminalis cDNA clone h37c06, mRNA sequence.
ACCESSION	CB076094
VERSION	CB076094.1
KEYWORDS	EST.
SOURCE	Hedyotis terminalis
ORGANISM	Hedyotis terminalis
REFERENCE	1 (bases 1 to 339)
AUTHORS	Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N., O'Shaughnessy,A.L., Ballja,V., Martienssen,R.A., McCombie,R.W., Benfey,P. and Stevenson,D.
TITLE	Expressed tag sequences from Hedyotis terminalis flower - Stage 2 (NYBG)
JOURNAL	Unpublished (2003)
COMMENT	Contact: W. Richard McCombie Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874

Email: mccombe@cshl.org
 Plate: hf37 row: c column: 06
 Seq primer: -21M13UnivRev
 High quality sequence stop: 339.
 Location/Qualifiers

FEATURES

source
 1..339
 /organism="Hedyotis terminalis"
 /mol_type="mRNA"
 /db_xref="taxon:219667"
 /clone="hf37c06"
 /dev_stage="pre-anthesis; Stage 2"
 /clone_lib="Hedyotis terminalis flower - Stage 2 (NYBG)"
 /note="Organ: flower; Vector: pBK-CMV; Site:1: XhoI;
 Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
 CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
 Synthesis Kit. The library was size-fractionated to enrich
 for large inserts. Sample: collected on the island of
 Hawaii, Hawaii; NYBG herbarium voucher TM2562"

ORIGIN

Query Match 92.0%; Score 18.4; DB 14; Length 339;
 Best Local Similarity 95.0%; Pred. No. 3.2e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 20
 ||||| ||||| ||||| |||||
 Db 99 GGTGCACCTGTCAGGGGG 80

RESULT 2

CB087291/c
 LOCUS 440 bp mRNA linear EST 27-JAN-2003
 DEFINITION hj98g11.g1 Hedyotis centranthoides flower - Stage 2 (NYBG) Hedyotis
 centranthoides cDNA clone hj98g11, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Hedyotis centranthoides
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Gentianales; Rubiaceae; Rubioideae;
 Spermacoceae; Hedyotis.

REFERENCE

AUTHORS

1 (bases 1 to 440)
 Levesque, M.P., Twigg, R.W., Motley, T., Katari, M.S., Dedhia, N.N.,
 O'Shaughnessy, A.L., Ballia, V., Martienssen, R.A., McCombie, R.W.,
 Benfey, P. and Stevenson, D.
 Expressed tag sequences from Hedyotis centranthoides flower - Stage
 2 (NYBG)

JOURNAL

COMMENT

Unpublished (2003)
 Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mccombe@cshl.org
 Plate: hf37 row: g column: 11
 Seq primer: -21M13UnivRev
 High quality sequence stop: 440.
 Location/Qualifiers

FEATURES

source

1..440
 /organism="Hedyotis centranthoides"
 /mol_type="mRNA"
 /db_xref="taxon:219666"
 /clone="hj98g11"
 /dev_stage="pre-anthesis; Stage 2"
 /clone_lib="Hedyotis centranthoides flower - Stage 2
 (NYBG)"
 /note="Organ: flower; Vector: pBK-CMV; Site:1: XhoI;
 Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
 CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
 Synthesis Kit. The library was size-fractionated to enrich
 for large inserts. Sample: collected on the island of
 Hawaii, Hawaii; NYBG herbarium voucher TM2563"

for large inserts. Sample: collected on the island of
 Hawaii, Hawaii; NYBG herbarium voucher TM2563"

ORIGIN

Query Match 92.0%; Score 18.4; DB 14; Length 440;
 Best Local Similarity 95.0%; Pred. No. 3.3e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 20
 ||||| ||||| ||||| |||||
 Db 131 GGTGCACCTGTCAGGGGG 112

RESULT 3

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Hedyotis centranthoides

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamids; Gentianales; Rubiaceae; Rubioideae;

Spermacoceae; Hedyotis.

REFERENCE

AUTHORS

1 (bases 1 to 509)

Levesque, M.P., Twigg, R.W., Motley, T., Katari, M.S., Dedhia, N.N.,

O'Shaughnessy, A.L., Ballia, V., Martienssen, R.A., McCombie, R.W.,

Benfey, P. and Stevenson, D.

Expressed tag sequences from Hedyotis centranthoides flower - Stage

2 (NYBG)

Unpublished (2003)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mccombe@cshl.org

Plate: hf97 row: e column: 04

Seq primer: -21M13UnivRev

High quality sequence stop: 509.

Location/Qualifiers

1..509

/organism="Hedyotis centranthoides"

/mol_type="mRNA"

/db_xref="taxon:219666"

/clone="hj97e04"

/dev_stage="pre-anthesis; Stage 2"

/clone_lib="Hedyotis centranthoides flower - Stage 2

(NYBG)"

/note="Organ: flower; Vector: pBK-CMV; Site:1: XhoI;

Site 2: Eco RI; Date: Completed 12/18/01. Submitted to

CSHL 12/21/01 Library: Stratagene ZAP Express cDNA

Synthesis Kit. The library was size-fractionated to enrich

for large inserts. Sample: collected on the island of

Hawaii, Hawaii; NYBG herbarium voucher TM2563"

RESULT 4

LOCUS

CB087525/c

LOCUS

598 bp mRNA linear EST 27-JAN-2003

```

DEFINITION   hk03f05.g1 Hedyotis centranthoides flower - Stage 2 (NYBG) Hedyotis
              centranthoides cDNA clone hk03f05, mRNA sequence.
ACCESSION    CB087525
VERSION      CB087525.1  GI:27911717
KEYWORDS     EST.
SOURCE       Hedyotis centranthoides
              Hedyotis centranthoides
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              asterids; lamids; Gentianales; Rubiaceae; Rubioideae;
              Spermaceae; Hedyotis.
REFERENCE    1 (bases 1 to 598)
AUTHORS      Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N.,
              O'Shaughnessy,A.L., Ballija,V., Martienssen,R.A., McCombie,R.W.,
              Benfey,P. and Stevenson,D.
              Expressed tag sequences from Hedyotis centranthoides flower - Stage
              2 (NYBG)
JOURNAL      Unpublished (2003)
COMMENT      Contact: W. Richard McCombie
              Lita Annenberg Hazen Genome Sequencing Center
              Cold Spring Harbor Laboratory
              PO Box 100, Cold Spring Harbor, NY 11724, USA
              Tel: 516 367 8884
              Fax: 516 367 8874
              Email: mcombie@cshl.org
              Plate: hk03 row: f column: 05
              Seq primer: -21M13UnivRev
              High quality sequence stop: 598.
              Location/Qualifiers
              1..598
                /organism="Hedyotis centranthoides"
                /mol_type="mRNA"
                /db_xref="taxon:219666"
                /clone="hk03f05"
                /dev_stage="pre-anthesis; Stage 2"
                /clone_lib="Hedyotis centranthoides flower - Stage 2
              (NYBG)"
                /note="Organ: flower; Vector: pSK-CMV; Site:1: XhoI;
              Site:2: Eco RI; Date: Completed 12/18/01. Submitted to
              CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
              Synthesis kit. The library was size-fractionated to enrich
              for large inserts. Sample: collected on the island of
              Hawaii, Hawaii; NYBG herbarium voucher TW2563"
ORIGIN
  Query Match      92.0%; Score 18.4; DB 14; Length 598;
  Best Local Similarity 95.0%; Pred. No. 3.4e+03;
  Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  QY 1 GGTGCACCGGTGCAGGGGG 20
      |||||
  Db 148 GGTGCACCGGTGCAGGGGG 129

RESULT 5
CG271799
LOCUS       CG271799
DEFINITION CG271799 840 bp DNA linear GSS 25-AUG-2003
              CG00D226TV_ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0696F04,
              genomic survey sequence.
ACCESSION   CG271799
VERSION     CG271799.1  GI:34183940
KEYWORDS    GSS.
SOURCE      Zea mays
              Zea mays
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
              1 (bases 1 to 840)
REFERENCE   1 (bases 1 to 840)
AUTHORS     Whitelaw,C.A., Quackenbush,J.J., Van Aken,S., Utterback,T.,
              Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
              Cicek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
              Consortium for Maize Genomics
              Unpublished (2002)
              Location/Qualifiers
              1..840
                /organism="Zea mays subsp. mays"
                /mol_type="genomic DNA"
                /cultivar="B73"
                /sub_species="mays"
                /db_xref="taxon:4578"
                /clone="ZMMBMA0696F04"
                /lab_host="DH10B"
                /clone_lib="ZMMBMA0696F04"
                /note="vector: pBESBAC11; Site_1: HindIII; Site_2:

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```

COMMENT      Other_GSSs: OG0D226TH
              TIGR
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301-838-5843
              Fax: 301-838-0208
              Email: whitelaw@tigr.org
              Seq primer: 1F
              Class: sheared ends.
              Location/Qualifiers
              1..840
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /strain="B73"
                /db_xref="taxon:4577"
                /clone="ZMMBMA0696F04"
                /clone_lib="ZM 0.7 1.5 KB"
                /note="vector: pBESK-; Site 1: HincII; 0.7-1.5 kb
              methylation filtered genomic DNA library"
FEATURES
  source
  1..840
  Query Match      92.0%; Score 18.4; DB 29; Length 840;
  Best Local Similarity 95.0%; Pred. No. 3.5e+03;
  Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  QY 1 GGTGCACCGGTGCAGGGGG 20
      |||||
  Db 499 GGTGCACCGGTGCAGGGGG 518

RESULT 6
CG692380
LOCUS       CG692380
DEFINITION ZMMBMA0292G11.f ZMMBMA Zea mays subsp. mays genomic clone
              ZMMBMA0292G11 5', genomic survey sequence.
ACCESSION   CG692380
VERSION     CG692380.1  GI:37656062
KEYWORDS    GSS.
SOURCE      Zea mays subsp. mays (maize)
              Zea mays subsp. mays
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
              1 (bases 1 to 610)
REFERENCE   1 (bases 1 to 610)
AUTHORS     Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
              and Wing,R.
              Sequencing of the maize genome
              Unpublished (2003)
              Contact: Rod Wing
              Arizona Genomics Institute
              University of Arizona
              Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
              85721-0088, USA
              Tel: 520 626 3967
              Fax: 520 621 9288
              Email: http://genome.arizona.edu
              PCR Primers
              FORWARD: T7
              BACKWARD: M13r
              Plate: 0292 row: G column: 13
              Seq primer: T7
              Class: BAC ends.
              Location/Qualifiers
              1..610
                /organism="Zea mays subsp. mays"
                /mol_type="genomic DNA"
                /cultivar="B73"
                /sub_species="mays"
                /db_xref="taxon:4578"
                /clone="ZMMBMA0292G11"
                /lab_host="DH10B"
                /clone_lib="ZMMBMA0292G11"
                /note="vector: pBESBAC11; Site_1: HindIII; Site_2:

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HindIII; Zea mays L. ssp. mays"

ORIGIN

Query Match 87.0%; Score 17.4; DB 29; Length 610;
 Best Local Similarity 94.7%; Pred. No. 8.3e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGCACCGGTGCAGGGGG 20
 |||||
 Db 524 GTGCACCGGTGCAGGGGG 542

RESULT 7

CC109078/c
 LOCUS NDL.50B23.T7 779 bp DNA linear GSS 16-APR-2003
 DEFINITION NDL.50B23.T7 Notre Dame Liverpool Aedes aegypti genomic clone
 CC109078 genomic survey sequence.

ACCESSION CC109078.1 GI:29978133

KEYWORDS GSS.

SOURCE Aedes aegypti (yellow fever mosquito)

ORGANISM

Aedes aegypti
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
 Stegomyia.

REFERENCE 1 (bases 1 to 779)

AUTHORS Loftus,B., Shetty,J., Knudson,D. and Severson,D.

TITLE BAC end sequencing of Aedes aegypti

JOURNAL Unpublished (2003)

COMMENT Other GSSs: NDL.50B23.SP6

Contact: Brendan Loftus

Department of Eukaryotic Genomics

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: entaetigr.org

Library was provided by David Severson

Seq primer: T7

Class: BAC ends.

FEATURES

source

1..779

/organism="Aedes aegypti"

/mol_type="genomic DNA"

/strain="liverpool"

/db_xref="taxon:7159"

/clone="NDL.50B23"

/clone_lib="Notre Dame Liverpool"

/notes="Vector: pECBAC1; Site_1: Hind III; The library was

prepared from whole body tissue of newly hatched L1 larvae

by David Severson at the University of Notre Dame and

Hongbin Zhang"

Query Match 87.0%; Score 17.4; DB 28; Length 779;

Best Local Similarity 94.7%; Pred. No. 8.5e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGCACCGGTGCAGGGGG 20

|||||

Db 307 GTGCACCGGTGCAGGGGG 289

RESULT 8

CC133230/c
 LOCUS NDL.50B22.T7 799 bp DNA linear GSS 16-APR-2003
 DEFINITION NDL.50B22.T7 Notre Dame Liverpool Aedes aegypti genomic clone
 CC133230 genomic survey sequence.

ACCESSION CC133230.1 GI:30002285

KEYWORDS GSS.

SOURCE Aedes aegypti (yellow fever mosquito)

ORGANISM

Aedes aegypti

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
 Stegomyia.

1 (bases 1 to 799)

AUTHORS Loftus,B., Shetty,J., Knudson,D. and Severson,D.

TITLE BAC end sequencing of Aedes aegypti

JOURNAL Unpublished (2003)

COMMENT Other GSSs: NDL.50B22.SP6

Contact: Brendan Loftus

Department of Eukaryotic Genomics

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: entaetigr.org

Library was provided by David Severson

Seq primer: T7

Class: BAC ends.

FEATURES

source

1..799

/organism="Aedes aegypti"

/mol_type="genomic DNA"

/strain="liverpool"

/db_xref="taxon:7159"

/clone="NDL.50B22"

/clone_lib="Notre Dame Liverpool"

/notes="Vector: pECBAC1; Site_1: Hind III; The library was

prepared from whole body tissue of newly hatched L1 larvae

by David Severson at the University of Notre Dame and

Hongbin Zhang"

Query Match 87.0%; Score 17.4; DB 28; Length 799;

Best Local Similarity 94.7%; Pred. No. 8.5e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGCACCGGTGCAGGGGG 20

|||||

Db 307 GTGCACCGGTGCAGGGGG 289

RESULT 9

LOCUS

CNS04021

1005 bp DNA linear GSS 01-SEP-2000

DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone

073018 of library G from Tetraodon nigroviridis, genomic survey

sequence.

ACCESSION AL369542

VERSION AL369542.1 GI:7991434

KEYWORDS GSS; genome survey sequence.

SOURCE Tetraodon nigroviridis

ORGANISM Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorphi; Tetraodontiformes;

Tetraodontidae; Tetraodontinae; Tetraodon.

REFERENCE 1

AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,

Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,

Saurin,W. and Weissenbach,J.

TITLE Estimate of human gene number provided by genome-wide analysis

using Tetraodon nigroviridis DNA sequence

Nat. Genet. 25 (2), 235-238 (2000)

JOURNAL 20296633

MEDLINE 10835645

REFERENCE 2

AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,

Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,

Saurin,W., Bernot,A. and Weissenbach,J.

TITLE Characterization and repeat analysis of the compact genome of the

freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)

JOURNAL 20359837

MEDLINE

10899143
 REFERENCE 3 (bases 1 to 1005)
 Genoscope.
 AUTHORS Direct Submission
 TITLE Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetraodon nigroviridis
 genome. For more information, please take a look at
 http://www.genoscope.cns.fr/tetraodon.

FEATURES

source
 Location/Qualifiers
 1..1005
 /organism="Tetraodon nigroviridis"
 /mol_type="genomic DNA"
 /db_xref="taxon:9983"
 /clone="073018"
 /clone_lib="G"
 /note="Genoscope sequence ID : COBG073BH09SP1-end :
 PUC-Ori"

ORIGIN

Query Match 87.0%; Score 17.4; DB 29; Length 1005;
 Best Local Similarity 94.7%; Pred. No. 8.7e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 GTGCACCGGTGCAGGGGG 20
 Db 84 GTGCTCGGTGCAGGGGG 102

RESULT 10

BX426076
 LOCUS 1200 bp mRNA linear EST 15-MAY-2003
 DEFINITION BX426076 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 CSODF009YC20 5-PRIME, mRNA sequence.
 ACCESSION BX426076
 VERSION BX426076.1 GI:30774523
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1200)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 1373.1 For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0AAW152A08QP1&cluster=1373.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0AAW152A08QP1.

FEATURES

source
 Location/Qualifiers
 1..1200
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODF009YC20"
 /tissue_type="FETAL BRAIN"
 /dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Query Match 87.0%; Score 17.4; DB 13; Length 1200;
 Best Local Similarity 94.7%; Pred. No. 8.8e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GGTGCACCGGTGCAGGGGG 19
 Db 1117 GGGGACCGGTGCAGGGGG 1135

RESULT 11

BQ989390/c
 LOCUS 1214 bp mRNA linear EST 16-AUG-2002
 DEFINITION AGENCOURT 8712137 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6295181
 5' mRNA sequence.
 ACCESSION BQ989390
 VERSION BQ989390.1 GI:22290404
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1214)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LICM3501 row: a column: 06
 High quality sequence stop: 150.
 Location/Qualifiers
 1..1214
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6295181"
 /tissue_type="melanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_112"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

FEATURES

source
 Location/Qualifiers
 1..1214
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6295181"
 /tissue_type="melanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_112"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 87.0%; Score 17.4; DB 13; Length 1214;
 Best Local Similarity 94.7%; Pred. No. 8.8e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 19

Db 301 GGTGCACCGGTGCAGGGGG 283

RESULT 12

AV393217/c
 LOCUS 354 bp mRNA linear EST 23-APR-2002
 DEFINITION AV393217 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii
 cDNA clone CM097f03_r 5', mRNA sequence.
 ACCESSION AV393217
 VERSION AV393217.1 GI:6547433

```

KEYWORDS
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
REFERENCE 1 (bases 1 to 354)
AUTHORS Asamizu, S., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S.
TITLE A large scale structural analysis of cDNAs in a unicellular green
        alga, Chlamydomonas reinhardtii. I. Generation of 3433
        non-redundant expressed sequence tags
JOURNAL DNA Res. 6 (6), 369-373 (1999)
MEDLINE 20152988
PUBMED 10691129
COMMENT Contact: Yasukazu Nakamura
        The First Laboratory for Plant Gene Research
        Kazusa DNA Research Institute
        Yana 1532-3, Kisarazu, Chiba 252-0812, Japan
        Email: ynakam@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
        source
            1..354
                /organism="Chlamydomonas reinhardtii"
                /mol_type="cDNA"
                /strain="C9"
                /db_xref="taxon:3055"
                /clone="CM097F03 r"
                /dev_stage="photoautotrophic growth"
                /clone_lib="Chlamydomonas reinhardtii C9"
                /note="Vector: pBluescriptII SK; Site_1: EcoRI; Site_2:
                XhoI"
ORIGIN
Query Match 85.0%; Score 17; DB 9; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTGCACCGGTGCAGGG 17
    |||||
Db 310 GGTGCACCGGTGCAGGG 294
RESULT 13
LOCUS BE388878 142 bp mRNA linear EST 21-JUL-2000
DEFINITION 601284657F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606422 5',
mRNA sequence.
ACCESSION BE388878
VERSION BE388878.1 GI:9334243
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 142)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM256 row: a column: 15
High quality sequence start: 2
High quality sequence stop: 18.
FEATURES
        source
            1..142
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
/clone="IMAGE:3606422"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_44"
/notes="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

```

Query Match 84.0%; Score 16.8; DB 10; Length 142;
Best Local Similarity 90.0%; Pred. No. 1.3e+04;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGTGCACCGGTGCAGGGGGG 20
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Db 109 GGTGCACCGGTGCAGGGGAG 128
```

RESULT 14

```

AZ492326/c
LOCUS AZ492326 237 bp DNA linear GSS 05-OCT-2000
DEFINITION IM0326G23F Mouse 10kb plasmid UUC1M library Mus musculus genomic
        clone UUC1M0326G23 F, genomic survey sequence.
ACCESSION AZ492326
VERSION AZ492326.1 GI:10664936
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 237)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
        Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
        Reilly, M., Rose, R., Stokes, R., Tingey, A., von
        Niederhausern, A. and Wright, D., Weiss, R.
        Mouse whole genome scaffolding with paired end reads from 10kb
        plasmid inserts
        Unpublished (2000)
        Contact: Robert B. Weiss
        University of Utah Genome Center
        Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
        84112, USA
        Tel: 801 585 5606
        Fax: 801 585 7177
        Email: daune@genetics.utah.edu
        Insert Length: 10000 Std Error: 0.00
        Plate: 0326 row: G column: 23
        Seq primer: CGTTGTAACACGCGCCAGT
        Class: plasmid ends
        High quality sequence stop: 237.
        Location/Qualifiers
            1..237
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUC1M0326G23"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUC1M library"
                /note="Vector: pMD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
```

FEATURES

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        source
```

ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G[4732114]g[Ar29072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 84.0%; Score 16.8; DB 28; Length 237;
Best Local Similarity 90.0%; Pred. No. 1.3e+04;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 20

Db 100 GGTGCACCGGTGCAGGGGG 81

RESULT 15
LOCUS BB496626 275 bp mRNA linear EST 26-JUL-2000
DEFINITION BB496626 RIKEN full-length enriched, 0 day neonate kidney Mus musculus cDNA clone D63004A12 3' similar to X52101 Mouse mRNA for a 25kDa nuclear protein found in murine plasmacytoma, mRNA sequence.

ACCESSION BB496626

VERSION BB496626

KEYWORDS BB496626

SOURCE BB496626.1 GI:9469711

ORGANISM Mus musculus (house mouse)

REFERENCE Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 275)

AUTHORS

Konno.H., Aizawa.K., Akahira.S., Akiyama.J., Arakawa.T., Carninci.P., Endo.T., Fukuda.S., Fukunishi.Y., Hara.A., Hayatsu.N., Hirozane.T., Hori.F., Ishii.Y., Ishikawa.J., Ishikawa.T., Itoh.M., Izawa.M., Kadota.K., Kagawa.I., Kai.C., Kawai.J., Kikuchi.N., Kiyosawa.H., Kojima.Y., Kondo.S., Koya.S., Kurihara.C., Kusakabe.M., Matsuyama.T., Miki.R., Mizuno.Y., Nakamura.M., Oda.H., Okazaki.Y., Ono.T., Owa.C., Saito.H., Sakai.C., Sato.K., Shibata.K., Shibata.Y., Shigemoto.Y., Shinagawa.A., Shiraki.T., Sogabe.Y., Sugahara.Y., Suzuki.H., Suzuki.H., Tagawa.A., Watanabe.S., Yamamura.T., Yamanaka.I., Yano.R., Yasunishi.A., Yokota.T., Yoshida.K., Yoshiki.A., Yoshino.M., Muramatsu.M. and Hayashizaki.Y.

RIKEN Mouse ESTs (Konno.H., et al.)

Unpublished (2000)

JOURNAL

Contact: Yoshihide Hayashizaki
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp

URL: http://genome.gsc.riken.go.jp/

Carninci.P., Nishiyama.Y., Westover.A., Itoh.M., Nagaoka.S., Sasaki.N., Okazaki.Y., Muramatsu.M. and Hayashizaki.Y.
Thermotabilization and thermoactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2): 520-524 (1998)
Itoh.M., Kiteunai.T., Akiyama.J., Shibata.K., Izawa.M., Kawai.J., Tomaru.Y., Carninci.P., Shibata.Y., Ozawa.Y., Muramatsu.M., Okazaki.Y. and Hayashizaki.Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5): 463-470 (1999)
Carninci.P. and Hayashizaki.Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,

19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers
1..275
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clones="D630004A12"
/tissue_type="kidney"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 0 day neonate kidney"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGCGCGCCGACCTCGAGTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGTTCTCGAGTTTCTTTTNN 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda PLC I."

ORIGIN

Query Match 84.0%; Score 16.8; DB 10; Length 275;

Best Local Similarity 90.0%; Pred. No. 1.3e+04;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 20

Db 152 GGTGCACCGGTGCAGGGGG 171

Search completed: July 2, 2004, 13:32:53

Job time : 1500.92 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 06:05:50 ; Search time 134.89 Seconds
(without alignments)

566.887 Million cell updates/sec

Title: US-10-068-160-13

Perfect score: 18

Sequence: 1 tgcaccggtgcagg9999 18

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 29Jan04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002s:*

7: geneseqn2003as:*

8: geneseqn2003bs:*

9: geneseqn2003cs:*

10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	20	4 AAC80622	AAC80622 Immunogen
2	18	100.0	20	4 AAS09592	AAS09592 Immunorea
3	18	100.0	20	6 ABL35614	ABL35614 Immunosti
4	18	100.0	20	6 ABL35578	ABL35578 Immunosti
5	18	100.0	20	6 ABL35581	ABL35581 Immunosti
6	18	100.0	20	6 ABL35570	ABL35570 Immunosti
7	18	100.0	20	6 ABL35588	ABL35588 Immunosti
8	18	100.0	20	6 ABK46470	ABK46470 Immunosti
9	18	100.0	20	7 ACC48296	ACC48296 CpG oligo
10	18	100.0	20	7 ACC48300	ACC48300 CpG oligo
11	18	100.0	20	7 ACC48313	ACC48313 CpG oligo
12	18	100.0	20	8 ACC83118	ACC83118 D class C
13	18	100.0	20	8 ACC83152	ACC83152 D class C
14	18	100.0	20	9 ADD01049	ADD01049 CpG D oli
15	18	100.0	28	6 ABL35599	ABL35599 Immunosti
16	18	100.0	28	6 ABL35603	ABL35603 Immunosti
17	18	100.0	28	6 ABL35591	ABL35591 Immunosti
18	18	100.0	28	6 ABL35611	ABL35611 Immunosti
19	18	100.0	40	6 ABL35622	ABL35622 Immunosti
20	16.4	91.1	20	4 AAS09651	AAS09651 Immunorea
21	16.4	91.1	20	6 ABL35573	ABL35573 Immunosti
22	16.4	91.1	20	6 ABL35584	ABL35584 Immunosti
23	16.4	91.1	20	6 ABL35569	ABL35569 Immunosti

24	16.4	91.1	20	6 ABL35617	ABL35617 Immunosti
25	16.4	91.1	20	6 ABL35580	ABL35580 Immunosti
26	16.4	91.1	20	7 ACC48311	ACC48311 CpG oligo
27	16.4	91.1	20	7 ACC48320	ACC48320 CpG oligo
28	16.4	91.1	20	7 ACC48321	ACC48321 CpG oligo
29	16.4	91.1	20	8 ACC83125	ACC83125 D class C
30	16.4	91.1	20	8 ACC83116	ACC83116 D class C
31	16.4	91.1	20	8 ACC83126	ACC83126 D class C
32	16.4	91.1	20	9 ADD01076	ADD01076 CpG D oli
33	16.4	91.1	20	9 ADD01059	ADD01059 CpG D oli
34	16.4	91.1	28	6 ABL35590	ABL35590 Immunosti
35	16.4	91.1	28	6 ABL35594	ABL35594 Immunosti
36	16.4	91.1	28	6 ABL35606	ABL35606 Immunosti
37	16.4	91.1	28	6 ABL35602	ABL35602 Immunosti
38	15.4	85.6	19	4 AAC80602	AAC80602 Immunogen
39	15.4	85.6	19	4 AAS09572	AAS09572 Immunorea
40	15.4	85.6	19	6 ABK46450	ABK46450 Immunosti
41	15.4	85.6	278	5 ABA12385	ABA12385 Human ner
42	15.4	85.6	349	4 AAL01438	AAL01438 Human rep
43	15.4	85.6	349	4 ABL96885	ABL96885 Human tes
44	15.4	85.6	827	6 AAS61882	AAS61882 Porcine m
45	15	83.3	1466	5 AAS80037	AAS80037 DNA encod

ALIGNMENTS

RESULT 1

AAC80622 ID AAC80622 standard; DNA; 20 BP.

AC AAC80622;

DT 14-FEB-2001 (first entry)

DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:42.

KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response; vaccine;
KW B-cell response; antibody production; immune response induction; allergic
allergy; asthma; infection; bacterial; viral; fungal; protozoal;
parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
immune deficiency; biological warfare agent; cytostatic; antiarthritic;
antimicrobial; antiallergic; protozoicide; tuberculostatic;
antiasthmatic; dermatological; phosphorothioate; ss.

OS Synthetic.

XX WO200061151-A2.

XX 19-OCT-2000.

XX 12-APR-2000; 2000WO-US009839.

XX 12-APR-1999; 99US-0128898P.

XX (KLIN/) KLINMAN D.

XX (ISHI/) ISHII K.

XX (VERT/) VERTHELYI D.

XX Klinman D, Ishii K, Verthelyi D;

XX WPI, 2001-006880/01.

XX Novel oligonucleotides useful for the prevention and treatment of
allergies, cancer, and autoimmune disorders and for ameliorating symptoms
resulting from exposure to a bio-warfare agent.

XX Claim 4; Page 30; 46pp; English.

XX The invention relates to novel immunogenic CpG oligodeoxynucleotides

CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
 CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 CC -3'. The central CpG motif is unmodified, and the oligonucleotides
 CC optionally have phosphorothioate linkages which make them more resistant
 CC to degradation. The invention also relates to an oligonucleotide delivery
 CC complex comprising an oligonucleotide of the invention and a targeting
 CC agent, and a pharmaceutical composition comprising the oligonucleotide
 CC delivery complex. The oligonucleotides are able to induce either a cell-
 CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
 CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g., macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergenic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic
 CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antisense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention

XX SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
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 Db 3 TGCACCGGTGCAGGGGG 20

RESULT 2

AAS09592
 ID AAS09592 standard; DNA; 20 BP.

XX AAC09592;

XX 26-SEP-2001 (first entry)

XX Immunoreactive CpG sequence-containing oligonucleotide #42.

XX CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW leishmania; Ebola; Anthrax; Listeria; ss.

XX Synthetic.

XX WO200151500-A1.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-US001122.
 XX 14-JAN-2000; 2000US-0176115P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Klinman D, Ishii K, Verthelyi D;
 WPI; 2001-442129/47.

XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.

XX Claim 5; Page 34; 48pp; English.

XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria

XX SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
 |||||
 Db 3 TGCACCGGTGCAGGGGG 20

RESULT 3

ABL35614

XX ABL35614 standard; DNA; 20 BP.

XX ABL35614;

XX 04-APR-2002 (first entry)

XX Immunostimulatory oligonucleotide SEQ ID NO: 540.

XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
 KW infection; allergy; cancer; hypersensitivity; bio-warfare;
 KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
 KW immunosuppressive; protozoicide; virucide; hepatotropic; gene therapy;
 KW antinflammatory; antibacterial; ss.

XX Synthetic.

XX Key Location/Qualifiers

XX misc_RNA 1..20

```

FT      /tag= a
FT      /note= "optionally thymidine is replaced by uracil to
FT      form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT      least one other base through a ribose sugar"
XX
XX
PN      WO200193902-A2.
XX
XX      PD      13-DEC-2001.
XX
XX      PF      07-JUN-2001; 2001WO-US018276.
XX
XX      PR      07-JUN-2000; 2000US-0209797P.
XX
XX      PA      (BIOS-) BIOSYNEXUS INC.
XX
XX      PI      Mond JJ, Flora M, Klinman DM;
XX      DR      WPI; 2002-130570/17.
XX
XX      PT      New immunostimulatory compositions comprising RNA/DNA hybrid
XX      oligonucleotides, useful for enhancing an immune response or inducing
XX      cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX      HIV infection.
XX
XX      PS      Example 11; Page 62; 68pp; English.
XX
XX      CC      The present invention relates to an immunostimulatory composition, which
XX      comprises at least one oligonucleotide comprising both an RNA region and
XX      a DNA region. The composition is useful for enhancing an immune response
XX      or inducing cytokines. It can be used as a vaccine adjuvant and in
XX      treating diseases, including pathogenic infection, (non-)malignant
XX      tumors (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX      colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX      (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX      hepatitis, HIV or malaria. The composition is also useful for treating
XX      preventing or ameliorating the symptoms resulting from exposure to a bio-
XX      warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX      an immunostimulatory oligonucleotide described in the exemplification of
XX      the invention
XX
XX      SQ      Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match      100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGCACCGGTGCAGGGGG 18
        |||||
DB       3 TGCACCGGTGCAGGGGG 20

RESULT 4
ABL35578
ID      ABL35578 standard; DNA; 20 BP.
XX
XX      AC      ABL35578;
XX
XX      DT      04-APR-2002 (first entry)
XX
XX      DE      Immunostimulatory oligonucleotide SEQ ID NO: 504.
XX
XX      KW      DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX      infection; allergy; cancer; hypersensitivity; bio-warfare;
XX      immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX      immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX      antiinflammatory; antibacterial; ss.
XX
XX      OS      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      misc_RNA 1..20
XX      /tag= a
XX      /note= "optionally thymidine is replaced by uracil to
XX      form RNA or DNA/RNA hybrids. Thymidine is linked to at
XX      least one other base through a ribose sugar"

```

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FT      form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT      least one other base through a ribose sugar"
XX
XX      WO200193902-A2.
XX
XX      PD      13-DEC-2001.
XX
XX      PF      07-JUN-2001; 2001WO-US018276.
XX
XX      PR      07-JUN-2000; 2000US-0209797P.
XX
XX      PA      (BIOS-) BIOSYNEXUS INC.
XX
XX      PI      Mond JJ, Flora M, Klinman DM;
XX      DR      WPI; 2002-130570/17.
XX
XX      PT      New immunostimulatory compositions comprising RNA/DNA hybrid
XX      oligonucleotides, useful for enhancing an immune response or inducing
XX      cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX      HIV infection.
XX
XX      PS      Example 11; Page 61; 68pp; English.
XX
XX      CC      The present invention relates to an immunostimulatory composition, which
XX      comprises at least one oligonucleotide comprising both an RNA region and
XX      a DNA region. The composition is useful for enhancing an immune response
XX      or inducing cytokines. It can be used as a vaccine adjuvant and in
XX      treating diseases, including pathogenic infection, (non-)malignant
XX      tumors (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX      colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX      (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX      hepatitis, HIV or malaria. The composition is also useful for treating
XX      preventing or ameliorating the symptoms resulting from exposure to a bio-
XX      warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX      an immunostimulatory oligonucleotide described in the exemplification of
XX      the invention
XX
XX      SQ      Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match      100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGCACCGGTGCAGGGGG 18
        |||||
DB       3 TGCACCGGTGCAGGGGG 20

RESULT 5
ABL35581
ID      ABL35581 standard; DNA; 20 BP.
XX
XX      AC      ABL35581;
XX
XX      DT      04-APR-2002 (first entry)
XX
XX      DE      Immunostimulatory oligonucleotide SEQ ID NO: 507.
XX
XX      KW      DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX      infection; allergy; cancer; hypersensitivity; bio-warfare;
XX      immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX      immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX      antiinflammatory; antibacterial; ss.
XX
XX      OS      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      misc_RNA 1..20
XX      /tag= a
XX      /note= "optionally thymidine is replaced by uracil to
XX      form RNA or DNA/RNA hybrids. Thymidine is linked to at
XX      least one other base through a ribose sugar"

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XX PN WO200193902-A2.
XX PD
XX PF 13-DEC-2001.
XX PR
XX PR 07-JUN-2001; 2001WO-US018276.
XX PR 07-JUN-2000; 2000US-0209797P.
XX PR (BIOS-) BIOSYNEXUS INC.
XX PA
XX PI Mond JJ, Flora M, Klinman DM;
XX PI WPI; 2002-130570/17.
XX DR
XX DR New immunostimulatory compositions comprising RNA/DNA hybrid
XX PT oligonucleotides, useful for enhancing an immune response or inducing
XX PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX PT HIV infection.
XX PS
XX PS Example 11; Page 61; 68pp; English.
XX CC
XX CC The present invention relates to an immunostimulatory composition, which
XX CC comprises at least one oligonucleotide comprising both an RNA region and
XX CC a DNA region. The composition is useful for enhancing an immune response
XX CC or inducing cytokines. It can be used as a vaccine adjuvant and in
XX CC treating diseases, including pathogenic infection, (non-)malignant
XX CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX CC hepatitis, HIV or malaria. The composition is also useful for treating,
XX CC preventing or ameliorating the symptoms resulting from exposure to a bio-
XX CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX CC an immunostimulatory oligonucleotide described in the exemplification of
XX CC the invention
XX SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 6
ABL35570
ID ABL35570 standard; DNA; 20 BP.
XX AC
XX AC ABL35570;
XX DT 04-APR-2002 (first entry)
XX DE
XX DE Immunostimulatory oligonucleotide SEQ ID NO: 496.
XX KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX KW infection; allergy; cancer; hypersensitivity; bio-warfare;
XX KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX KW antiinflammatory; antibacterial; ss.
XX OS
XX OS Synthetic.
XX PH
XX PH Key Location/Qualifiers
XX FT misc_RNA 1..20
XX FT /+tag= a
XX FT /note= "optionally thymidine is replaced by uracil to
XX FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
XX FT least one other base through a ribose sugar"
XX PN WO200193902-A2.

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XX PD 13-DEC-2001.
XX PF 07-JUN-2001; 2001WO-US018276.
XX PR 07-JUN-2000; 2000US-0209797P.
XX PR (BIOS-) BIOSYNEXUS INC.
XX PA
XX PI Mond JJ, Flora M, Klinman DM;
XX PI WPI; 2002-130570/17.
XX DR
XX DR New immunostimulatory compositions comprising RNA/DNA hybrid
XX PT oligonucleotides, useful for enhancing an immune response or inducing
XX PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX PT HIV infection.
XX PS
XX PS Example 11; Page 61; 68pp; English.
XX CC
XX CC The present invention relates to an immunostimulatory composition, which
XX CC comprises at least one oligonucleotide comprising both an RNA region and
XX CC a DNA region. The composition is useful for enhancing an immune response
XX CC or inducing cytokines. It can be used as a vaccine adjuvant and in
XX CC treating diseases, including pathogenic infection, (non-)malignant
XX CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX CC hepatitis, HIV or malaria. The composition is also useful for treating,
XX CC preventing or ameliorating the symptoms resulting from exposure to a bio-
XX CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX CC an immunostimulatory oligonucleotide described in the exemplification of
XX CC the invention
XX SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 7
ABL35588
ID ABL35588 standard; DNA; 20 BP.
XX AC
XX AC ABL35588;
XX DT 04-APR-2002 (first entry)
XX DE
XX DE Immunostimulatory oligonucleotide SEQ ID NO: 514.
XX KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX KW infection; allergy; cancer; hypersensitivity; bio-warfare;
XX KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX KW antiinflammatory; antibacterial; ss.
XX OS
XX OS Synthetic.
XX PH
XX PH Key Location/Qualifiers
XX FT misc_RNA 1..20
XX FT /+tag= a
XX FT /note= "optionally thymidine is replaced by uracil to
XX FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
XX FT least one other base through a ribose sugar"
XX PN WO200193902-A2.
XX PD 13-DEC-2001.

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XX PF 07-JUN-2001; 2001WO-US018276.
XX PR 07-JUN-2000; 2000US-020979P.
XX PA (BIOS-) BIOSYNEXUS INC.
XX PI Mond JU, Flora M, Klinman DM;
XX DR WPI; 2002-227118/28.
XX CC Vaccine for immunizing patient against respiratory syncytial virus, has
XX PT epitopes of Paramyxoviridae P protein, and cytosine followed by guanine
XX PT linked by phosphate bond-oligodeoxynucleotides.
XX PS Claim 4; Page 8; 30pp; English.
XX CC The invention describes a vaccine comprising one or more epitopes of a
XX CC Paramyxoviridae P protein, and one or more CpG (cytosine followed by a
XX CC guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The
XX CC vaccine is useful for vaccinating a patient especially against viruses of
XX CC the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the
XX CC primary cause of viral bronchiolitis and pneumonia in infants and
XX CC children, and infectious pulmonary disease in infants. RSV has been
XX CC particularly implicated in death of infants that are premature, have
XX CC bronchopulmonary dysplasia, or congenital heart conditions. This sequence
XX CC represents an oligodeoxynucleotide that can be used in the creation of
XX CC the vaccine
XX SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 18; DB 6; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 64;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 TGCACCGGTGCAGGGGG 18
XX Db 3 TGCACCGGTGCAGGGGG 20
XX RESULT 9
XX ID ACC48296 standard; DNA; 20 BP.
XX AC ACC48296;
XX DT 11-AUG-2003 (first entry)
XX DE CpG oligodeoxynucleotide B29 used for dendritic cell maturation.
XX KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
XX KW cytostatic; immunostimulant; gene therapy; ss.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= phosphorothioate nucleotides"
XX FT modified_base 1
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= phosphorothioate nucleotide"
XX PN WO2003020884-A2.
XX OS
XX PD 13-MAR-2003.
XX PF 13-AUG-2002; 2002WO-US025732.
XX PR 14-AUG-2001; 2001US-0312190P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Klinman DM, Gursel M, Verthelyi D;
XX DR WPI; 2003-300874/29.
XX CC Generating mature dendritic cells for tumor immunotherapy or as vaccines
XX PT for activating the immune system to treat diseases such as cancer,
XX PT comprises contacting a dendritic cell precursor with a D type

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XX PF 07-JUN-2001; 2001WO-US018276.
XX PR 07-JUN-2000; 2000US-020979P.
XX PA (BIOS-) BIOSYNEXUS INC.
XX PI Mond JU, Flora M, Klinman DM;
XX DR WPI; 2002-130570/17.
XX CC New immunostimulatory compositions comprising RNA/DNA hybrid
XX CC oligonucleotides, useful for enhancing an immune response or inducing
XX CC cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX CC HIV infection.
XX PS Example 11; Page 61; 68pp; English.
XX CC The present invention relates to an immunostimulatory composition, which
XX CC comprises at least one oligonucleotide comprising both an RNA region and
XX CC a DNA region. The composition is useful for enhancing an immune response
XX CC or inducing cytokines. It can be used as a vaccine adjuvant and in
XX CC treating diseases, including pathogenic infection, (non-)malignant
XX CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX CC hepatitis, HIV or malaria. The composition is also useful for treating,
XX CC preventing or ameliorating the symptoms resulting from exposure to a bio-
XX CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX CC an immunostimulatory oligonucleotide described in the exemplification of
XX CC the invention
XX SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 18; DB 6; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 64;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 TGCACCGGTGCAGGGGG 18
XX Db 3 TGCACCGGTGCAGGGGG 20
XX RESULT 8
XX ID ABK46470 standard; DNA; 20 BP.
XX AC ABK46470;
XX DT 05-JUN-2002 (first entry)
XX DE Immunostimulatory unmethylated CpG oligodeoxynucleotide #60.
XX KW unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine;
XX KW Paramyxoviridae; P protein; respiratory syncytial virus; RSV;
XX KW viral bronchiolitis; pneumonia; infectious pulmonary disease;
XX KW bronchopulmonary dysplasia; congenital heart condition; ss.
XX OS Synthetic.
XX PN WO200211761-A2.
XX PD 14-FEB-2002.
XX PF 09-AUG-2001; 2001WO-US041633.
XX PR 10-SEP-2000; 2000US-0224011P.
XX PR 01-SEP-2000; 2000US-0229307P.
XX PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX PI Mond JU, Prince G, Klinman DM;
XX DR
XX CC

```

PT oligodeoxynucleotide.
PS Claim 11; Page 44; 69pp; English.
XX
CC The present sequence is that of D type CpG oligodeoxynucleotide D29,
CC which is used in a claimed method for generating a mature dendritic cell.
CC The method involves contacting a dendritic cell precursor, especially a
CC monocyte, with the oligonucleotide. The method is useful for generating
CC mature dendritic cells and enhancing T cell responses, thus enhancing
CC antigen presentation. Mature dendritic cells are useful for tumour
CC immunotherapy, for augmenting an immune response to an infectious agent
CC or to a vaccine, and as vaccines to prevent future infection or to
CC activate the immune system to treat diseases such as cancer. Mature
CC dendritic cells may also be used to produce activated T lymphocytes
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 10
ACC48300
ID ACC48300 standard; DNA; 20 BP.
XX
AC ACC48300;
XX
XX
DT 11-AUG-2003 (first entry)
XX
DE CpG oligodeoxynucleotide used for dendritic cell maturation.
XX
XX CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
KW cytostatic; immunostimulant; gene therapy; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1 /*tag= a
FT /*note= "N is any base (especially G) or no base"
FT misc_difference 2 /*tag= b
FT /*note= "N is any base (especially G) or no base"
FT
XX
PN WO2003020884-A2.
XX
XX
PD 13-MAR-2003.
XX
PP 13-AUG-2002; 2002WO-US025732.
XX
PR 14-AUG-2001; 2001US-0312190P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Gursel M, Verthelyi D;
XX
DR WPI; 2003-300874/29.
XX
XX Generating mature dendritic cells for tumor immunotherapy or as vaccines
PT for activating the immune system to treat diseases such as cancer,
PT comprises contacting a dendritic cell precursor with a D type
PT oligodeoxynucleotide.
XX
PS Disclosure; Page 26; 69pp; English.
XX
CC The present sequence is that of a D type CpG oligodeoxynucleotide that is
CC an example of claimed D type oligodeoxynucleotides (see ACC48294) of the
CC invention. Mature dendritic cells are obtained by contacting a dendritic

CC cell precursor, such as a monocyte, with such an oligodeoxynucleotide.
CC The method is useful for generating mature dendritic cells and enhancing
CC T cell responses, thus enhancing antigen presentation. Mature dendritic
CC cells are useful for tumour immunotherapy, for augmenting an immune
CC response to an infectious agent or to a vaccine, and as vaccines to
CC prevent future infection or to activate the immune system to treat
CC diseases such as cancer. Mature dendritic cells may also be used to
CC produce activated T lymphocytes
XX
SQ Sequence 20 BP; 2 A; 4 C; 10 G; 2 T; 0 U; 2 Other;

Query Match 100.0%; Score 18; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 11
ACC48313
ID ACC48313 standard; DNA; 20 BP.
XX
AC ACC48313;
XX
DT 11-AUG-2003 (first entry)
XX
DE CpG oligodeoxynucleotide.
XX
KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
KW cytostatic; immunostimulant; gene therapy; ss.
XX
OS Synthetic.
XX
PN WO2003020884-A2.
XX
PD 13-MAR-2003.
XX
PP 13-AUG-2002; 2002WO-US025732.
XX
PR 14-AUG-2001; 2001US-0312190P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Gursel M, Verthelyi D;
XX
DR WPI; 2003-300874/29.
XX
XX Generating mature dendritic cells for tumor immunotherapy or as vaccines
PT for activating the immune system to treat diseases such as cancer,
PT comprises contacting a dendritic cell precursor with a D type
PT oligodeoxynucleotide.
XX
PS Disclosure; Page 61; 69pp; English.
XX
CC The present sequence is that of a CpG oligodeoxynucleotide of the
CC invention. A claimed method for generating dendritic cells involves
CC contacting a dendritic cell precursor, especially a monocyte, with a D
CC type oligodeoxynucleotide (see ACC48294) containing a central
CC unmethylated CpG motif. The method is useful for generating mature
CC dendritic cells and enhancing T cell responses, thus enhancing antigen
CC presentation. Mature dendritic cells are useful for tumour immunotherapy,
CC for augmenting an immune response to an infectious agent or to a vaccine,
CC and as vaccines to prevent future infection or to activate the immune
CC system to treat diseases such as cancer. Mature dendritic cells may also
CC be used to produce activated T lymphocytes
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 TGCACCGGTGCAGGGGGG 18
DB 3 TGCACCGGTGCAGGGGGG 20

RESULT 12
ACC83118
ID ACC83118 standard; DNA; 20 BP.
XX
AC ACC83118;
XX
DT 27-AUG-2003 (first entry)
XX
DE D class CpG ODN sequence useful for encapsulating in SSCL, DV29.
XX
KW Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
KW tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
KW thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
KW schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
KW asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
KW CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
KW multiple sclerosis; infection; tumour; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
PN modified_base 16..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
PF WO2003040308-A2.
XX
PR 29-JUL-2002; 2002WO-US024235.
XX
PR 27-JUL-2001; 2001US-0308283P.
XX
PR 25-JUL-2002; 2002US-00206407.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK;
XX
DR WPI; 2003-482260/45.
XX
PT Cationic liposome composition for delivering oligodeoxynucleotides
PT including a CpG motif in clinical applications, comprises a cationic
PT lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
XX
PS Disclosure; Fig 10C; 110pp; English.
XX
CC The invention relates to sterically stabilised cationic liposomes (SSCL)
CC which comprises a cationic lipid, a co-lipid, stabilising agent and
CC encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.
CC The invention is useful in pharmaceutical composition for impairing
CC growth of a solid tumour cell (e.g. human tumour cell) bearing an
CC interleukin-13 receptor in a subject; for stimulating an immune response,
CC which is expression of a cytokine (e.g. interferon gamma), particularly
CC immunotherapeutic response against tumours or stimulating an in vivo or
CC an in vitro immune cell, and for inducing an immune response against an
CC infectious agent e.g. virus, bacteria and fungus. It is also useful for
CC delivering oligodeoxynucleotides including a CpG motif in clinical
CC applications; for treating infectious diseases (e.g. tularemia, malaria,
CC francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
CC (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer
CC etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,
CC bronchial or allergic asthma, urticaria, food allergies), autoimmune
CC diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and
CC multiple sclerosis) and psoriasis. The present sequence is a D class CpG
CC ODN potentially useful for encapsulating in SSCL
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match      100.0%; Score 18; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
   |||||
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 14
ADD01049
ID ADD01049 standard; DNA; 20 BP.
XX
AC ADD01049;
XX
DT 01-JAN-2004 (first entry)
DE
DE CpG D oligonucleotide SEQ ID NO:13.
XX
KW vascular endothelial growth factor; VEGF; CpG oligonucleotide;
KW neovascularisation; angiogenesis; vulnerability; vasotropic;
KW antiarteriosclerotic; gene therapy; skin graft; male pattern baldness;
KW atherosclerosis; ischaemia; ss.
XX
OS Synthetic.
XX
XX WO2003054161-A2.
XX
XX 03-JUL-2003.
XX
PF 18-DEC-2002; 2002WO-US040955.
XX
PR 20-DEC-2001; 2001US-0343457P.
XX
XX (UYTB-) UNIV TENNESSEE RES CORP.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Klinman DM, Zheng M, Rouse BT;
XX WPI; 2003-559138/52.
XX
XX Inducing the production of vascular endothelial growth factor by a cell,
XX useful for inducing angiogenesis, comprises contacting the cell with a
XX CpG oligodeoxynucleotide.
XX
XX Example 7; SEQ ID NO 13; 37pp; English.
XX
XX The present invention describes a method for inducing the production of
XX vascular endothelial growth factor (VEGF) by a cell comprising contacting
XX the cell with a CpG oligonucleotide and therefore inducing the production
XX of VEGF by the cell. Also described: (1) inducing neovascularisation in a
XX tissue, comprising introducing a CpG oligonucleotide into an area of the
XX tissue where the formation of new blood vessels is desired, and so
XX inducing neovascularisation in the area of the tissue; (2) promoting
XX angiogenesis in an area of the subject where angiogenesis is desired,
XX comprising introducing a CpG oligonucleotide to the area, and so
XX promoting angiogenesis in the subject; and (3) screening for an agent
XX that inhibits neovascularisation, comprising administering a CpG
XX oligonucleotide to a non-human mammal and administering the agent to the
XX mammal, where inhibition of angiogenesis in the animal indicates that the
XX agent is effective in inhibiting neovascularisation. The CpG
XX oligonucleotides have vulnerability, vasotropic and antiarteriosclerotic
XX activities, and can be used in gene therapy. The method and the CpG
XX oligonucleotides can be used in inducing angiogenesis or
XX neovascularisation, such as in subjects with a skin graft, subjects who
XX exhibit male pattern baldness, or subjects who have a wound or who have
XX atherosclerosis or ischaemia. The method may also be used in screening
XX for agents that inhibit neovascularisation. The present sequence
XX represents a CpG oligonucleotide which is used in the exemplification of
XX the present invention.
XX
XX Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
SQ

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Query Match      100.0%; Score 18; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
   |||||
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 15
ABL35599
ID ABL35599 standard; DNA; 28 BP.
XX
AC ABL35599;
XX
DT 04-APR-2002 (first entry)
DE
DE Immunostimulatory oligonucleotide SEQ ID NO: 525.
XX
KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW infection; allergy; cancer; hypersensitivity; bio-warfare;
KW immunostimulant; anti-allergic; cytostatic; antimicrobial; anti-HIV;
KW immunosuppressive; protozoicide; virucide; hepatotropic; gene therapy;
KW anti-inflammatory; antibacterial; ss.
XX
OS Synthetic.
XX
XX Location/Qualifiers
XX Key 1..28
XX misc_RNA /*tag= a
XX FT /note= "optionally thymidine is replaced by uracil to
XX FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
XX FT least one other base through a ribose sugar"
XX
XX WO200193902-A2.
XX
XX 13-DEC-2001.
XX
XX 07-JUN-2001; 2001WO-US018276.
XX
XX 07-JUN-2000; 2000US-0209797P.
XX (BIOS-) BIOSYNEXUS INC.
XX
XX Mond JJ, Flora M, Klinman DM;
XX WPI; 2002-130570/17.
XX
XX New immunostimulatory compositions comprising RNA/DNA hybrid
XX oligonucleotides, useful for enhancing an immune response or inducing
XX cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX HIV infection.
XX
XX Example 11; Page 61; 68pp; English.
XX
XX The present invention relates to an immunostimulatory composition, which
XX comprises at least one oligonucleotide comprising both an RNA region and
XX a DNA region. The composition is useful for enhancing an immune response
XX or inducing cytokines. It can be used as a vaccine adjuvant and in
XX treating diseases, including pathogenic infection (non-malignant
XX tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX hepatitis, HIV or malaria. The composition is also useful for treating,
XX preventing or ameliorating the symptoms resulting from exposure to a bio-
XX warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX an immunostimulatory oligonucleotide described in the exemplification of
XX the invention
XX
XX Sequence 28 BP; 10 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
SQ

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Best Local Similarity 100.0%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3 TGCACCGGTGCACGGGGG 20

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Job time : 135.89 secs

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Run on: July 2, 2004, 07:36:05 ; Search time 633.732 Seconds
(without alignments)
1231.080 Million cell updates/sec

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Perfect score: 18
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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8: gb.pl.*
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12: gb.sy.*
13: gb.un.*
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17: em.hum.*
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20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.roi.*
27: em.sts.*
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35: em.htg.rod.*
36: em.htg.nam.*
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40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	18	100.0	20	6	AX194442	AX194442 Sequence
2	18	100.0	20	6	AX352200	AX352200 Sequence
3	18	100.0	20	6	AX352208	AX352208 Sequence
4	18	100.0	20	6	AX352211	AX352211 Sequence
5	18	100.0	20	6	AX352218	AX352218 Sequence
6	18	100.0	20	6	AX352244	AX352244 Sequence
7	18	100.0	20	6	AX465392	AX465392 Sequence
8	18	100.0	28	6	AX352221	AX352221 Sequence
9	18	100.0	28	6	AX352229	AX352229 Sequence
10	18	100.0	28	6	AX352233	AX352233 Sequence
11	18	100.0	28	6	AX352241	AX352241 Sequence
12	18	100.0	40	6	AX352252	AX352252 Sequence
13	17	94.4	10782	1	AE001002	AE001002 Archaeogl
14	16.4	91.1	20	6	AX194501	AX194501 Sequence
15	16.4	91.1	20	6	AX352199	AX352199 Sequence
16	16.4	91.1	20	6	AX352203	AX352203 Sequence
17	16.4	91.1	20	6	AX352210	AX352210 Sequence
18	16.4	91.1	20	6	AX352214	AX352214 Sequence
19	16.4	91.1	20	6	AX352247	AX352247 Sequence
20	16.4	91.1	28	6	AX352220	AX352220 Sequence
21	16.4	91.1	28	6	AX352224	AX352224 Sequence
22	16.4	91.1	28	6	AX352232	AX352232 Sequence
23	16.4	91.1	28	6	AX352236	AX352236 Sequence
24	16.4	91.1	124270	10	AC091518	AC091518 Mus muscu
25	16.4	91.1	155724	4	AC091316	AC091316 Sus scro
26	16.4	91.1	201320	2	AC073816	AC073816 Mus muscu
27	16.4	91.1	260424	2	AC131745	AC131745 Mus muscu
28	16.4	91.1	307820	2	AC130831	AC130831 Mus muscu
29	16.4	91.1	347365	1	BX569691	BX569691 Synchoco
30	16	88.9	13787	1	AE013603	AE013603 Yersinia
31	16	88.9	47225	2	AC099869	AC099869 Mus muscu
32	16	88.9	110000	2	AC105643	Continuation (5 of
33	16	88.9	210644	2	AC116555	AC116555 Mus muscu
34	16	88.9	230500	1	AF414158	AF414158 Yersinia
35	16	88.9	240918	2	AC137254	AC137254 Rattus no
36	16	88.9	264464	2	AC107410	AC107410 Rattus no
37	16	88.9	323991	2	AC098512	AC098512 Rattus no
38	15.4	85.6	19	6	AX194422	AX194422 Sequence
39	15.4	85.6	19	6	AX465372	AX465372 Sequence
40	15.4	85.6	342	11	AU027239	AU027239 Rattus no
41	15.4	85.6	540	4	AY316132	AY316132 Felis cat
42	15.4	85.6	827	6	AX283735	AX283735 Sequence
43	15.4	85.6	1236	14	AF082811	AF082811 Cercopith
44	15.4	85.6	1245	14	AF082813	AF082813 Cercopith
45	15.4	85.6	1246	14	AF082814	AF082814 Cercopith

ALIGNMENTS

RESULT 1	AX194442	Sequence 42 from Patent WO0151500.	20 bp	DNA	linear	PAT 28-AUG-2001
LOCUS	AX194442	Sequence 42 from Patent WO0151500.				
DEFINITION	AX194442					
ACCESSION	AX194442					
VERSION	AX194442.1	GI:15385098				
KEYWORDS		synthetic construct				
SOURCE		synthetic construct				
ORGANISM		artificial sequences.				
REFERENCE	1					
AUTHORS		Klinman, D., Ishii, K. and Verthelyi, D.				
TITLE		Oligodeoxynucleotide and its use to induce an immune response				
JOURNAL		Patent: WO 0151500-A 42 19-JUL-2001;				
		Secretary of the Department of Health and Human Services (US)				


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AX352244      AX352244      20 bp      DNA      linear      PAT 06-FEB-2002
LOCUS
DEFINITION   Sequence 540 from Patent WO0193902.
ACCESSION   AX352244
VERSION     AX352244.1  GI:18617527
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    .
REFERENCE   1
AUTHORS     Mond,J.J., Flora,M. and Klinman,D.M.
TITLE       Immunostimulatory rna/dna hybrid molecules
JOURNAL     Patent: WO 0193902-A 540 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES    Location/Qualifiers
            source
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic HDR"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
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Db 3 TGCACCGGTGCAGGGGG 20

RESULT 7
AX465392      AX465392      20 bp      DNA      linear      PAT 16-JUL-2002
LOCUS
DEFINITION   Sequence 60 from Patent WO0211761.
ACCESSION   AX465392
VERSION     AX465392.1  GI:21899755
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    .
REFERENCE   1
AUTHORS     Mond,J.J., Prince,G. and Klinman,D.M.
TITLE       Vaccine against RSV
JOURNAL     Patent: WO 0211761-A 60 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES    Location/Qualifiers
            source
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic oligonucleotide"
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
    |||||
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 8
AX352221      AX352221      28 bp      DNA      linear      PAT 06-FEB-2002
LOCUS
DEFINITION   Sequence 517 from Patent WO0193902.
ACCESSION   AX352221
VERSION     AX352221.1  GI:18617504
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    .
REFERENCE   1
AUTHORS     Mond,J.J., Flora,M. and Klinman,D.M.
TITLE       Immunostimulatory rna/dna hybrid molecules
JOURNAL     Patent: WO 0193902-A 529 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES    Location/Qualifiers
            source
            1..28
            /organism="synthetic construct"

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artificial sequences.
REFERENCE   1
AUTHORS     Mond,J.J., Flora,M. and Klinman,D.M.
TITLE       Immunostimulatory rna/dna hybrid molecules
JOURNAL     Patent: WO 0193902-A 517 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES    Location/Qualifiers
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            /organism="synthetic construct"
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Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
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Db 3 TGCACCGGTGCAGGGGG 20

RESULT 9
AX352229      AX352229      28 bp      DNA      linear      PAT 06-FEB-2002
LOCUS
DEFINITION   Sequence 525 from Patent WO0193902.
ACCESSION   AX352229
VERSION     AX352229.1  GI:18617512
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    .
REFERENCE   1
AUTHORS     Mond,J.J., Flora,M. and Klinman,D.M.
TITLE       Immunostimulatory rna/dna hybrid molecules
JOURNAL     Patent: WO 0193902-A 525 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES    Location/Qualifiers
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            /db_xref="taxon:32630"
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Query Match      100.0%; Score 18; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
    |||||
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 10
AX352233      AX352233      28 bp      DNA      linear      PAT 06-FEB-2002
LOCUS
DEFINITION   Sequence 529 from Patent WO0193902.
ACCESSION   AX352233
VERSION     AX352233.1  GI:18617516
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    .
REFERENCE   1
AUTHORS     Mond,J.J., Flora,M. and Klinman,D.M.
TITLE       Immunostimulatory rna/dna hybrid molecules
JOURNAL     Patent: WO 0193902-A 529 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES    Location/Qualifiers
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            /organism="synthetic construct"

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
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Db 16 TGCACCGGTGCAGGGGG 33

RESULT 13
AE001002
LOCUS      Archaeoglobus fulgidus DSM 4304 section 105 of the complete
DEFINITION Archaeoglobus fulgidus DSM 4304 section 105 of the complete
           genome.
ACCESSION  AE001002 AE000782
VERSION     AE001002.1 GI:2689325
KEYWORDS
SOURCE      Archaeoglobus fulgidus DSM 4304
ORGANISM    Archaeoglobus fulgidus DSM 4304
            Archaeoglobus fulgidus DSM 4304
            Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
            Archaeoglobaceae; Archaeoglobus.
REFERENCE   1 (bases 1 to 10782)
AUTHORS     Klenk,H.P., Clayton,R.A., Tomb,J., White,O., Nelson,K.E.,
            Richardson,D.L., Kerlavage,A.R., Gwinn,M., Hickey,E.K., Peterson,J.D.,
            Fleischmann,R.D., Quackenbush,J., Lee,N.H., Sutton,G.G., Gill,S.,
            Kirkness,E.F., Dougherty,B.A., McKenney,K., Adams,M.D., Loftus,B.,
            Peterson,S., Reich,C.I., McNeil,L.K., Badger,J.H., Glodek,A.,
            Zhou,L., Overbeek,R., Gocayne,J.D., Weidman,J.F., McDonald,L.,
            Uterback,T., Cotton,M.D., Spriggs,T., Artiach,P., Kaine,B.P.,
            Sykes,S.M., Sadow,P.W., D'Andrea,K.P., Bowman,C., Fujii,C.,
            Garland,S.A., Mason,T.M., Olsen,G.J., Fraser,C.M., Smith,H.O.,
            Woese,C.R. and Venter,J.C.
TITLE       The complete genome sequence of the hyperthermophilic,
            sulphate-reducing archaeon Archaeoglobus fulgidus
JOURNAL     Nature 390 (6658), 364-370 (1997)
MEDLINE     98049343
PUBMED      9389475
REFERENCE   2 (bases 1 to 10782)
AUTHORS     Klenk,H.P., Clayton,R.A., Tomb,J.-F., White,O., Nelson,K.E.,
            Ketchum,K.A., Dodson,R.J., Gwinn,M., Hickey,E.K., Peterson,J.D.,
            Richardson,D.L., Kerlavage,A.R., Graham,D.E., Kyripides,N.C.,
            Fleischmann,R.D., Quackenbush,J., Lee,N.H., Sutton,G.G., Gill,S.,
            Kirkness,E.F., Dougherty,B.A., McKenney,K., Adams,M.D., Loftus,B.,
            Peterson,S., Reich,C.I., McNeil,L.K., Badger,J.H., Glodek,A.,
            Zhou,L., Overbeek,R., Gocayne,J.D., Weidman,J.F., McDonald,L.,
            Uterback,T., Cotton,M.D., Spriggs,T., Artiach,P., Kaine,B.P.,
            Sykes,S.M., Sadow,P.W., D'Andrea,K.P., Bowman,C., Fujii,C.,
            Garland,S.A., Mason,T.M., Olsen,G.J., Fraser,C.M., Smith,H.O.,
            Woese,C.R. and Venter,J.C.
TITLE       Direct Submission
JOURNAL     Submitted (15-DEC-1997) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA
REMARK      In order to show the genes in ascending order on the genome, the
            origin of this version has been moved by TIGR to position 2093570
            of the original version and the opposite strand is shown from the
            original version.
COMMENT      On Dec 16, 1997 this sequence version replaced gi:2649104.
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ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
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Db 11 TGCACCGGTGCAGGGGG 28

RESULT 11
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LOCUS      Sequence 537 from Patent WO0193902.
DEFINITION
ACCESSION  AX352241
VERSION     AX352241.1 GI:18617524
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Mond,J.J., Flora,M. and Klinman,D.M.
TITLE       Immunostimulatory rna/dna hybrid molecules
JOURNAL     Patent: WO 0193902-A 537 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES     Location/Qualifiers
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                /note="Synthetic HDR"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
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Db 11 TGCACCGGTGCAGGGGG 28

RESULT 12
AX352252
LOCUS      Sequence 548 from Patent WO0193902.
DEFINITION
ACCESSION  AX352252
VERSION     AX352252.1 GI:18617535
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Mond,J.J., Flora,M. and Klinman,D.M.
TITLE       Immunostimulatory rna/dna hybrid molecules
JOURNAL     Patent: WO 0193902-A 548 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES     Location/Qualifiers
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Query Match      100.0%; Score 18; DB 6; Length 40;
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/ cds="AF1459"
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putative"
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/ db_xref="GI:2649112"
/ translation="MPPMIPPKLPPEETIAEALYSSIIIFLCFLIYHRLREVYKLS
DYRGPHFFNTFLFGLVPLFVLLSASGVWPFBIISDEGLRGIMAFSGMFLAYAS
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identified by sequence similarity; putative"
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/ protein_id="AAB89787.1"
/ db_xref="GI:2649108"
/ translation="WPLGDSVVVVFOISGICGTCVEVCPDVPFLEGGRAVIVWG"
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Best Local Similarity 100.0%; Pred. No. 6.5e-02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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DB 8164 TGCACCGGTGCAGGGGG 8180

RESULT 14
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Fri Jul 2 14:53:27 2004

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LOCUS AX194501 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 101 from Patent WO0151500.
ACCESSION AX194501
VERSION AX194501.1 GI:15385157
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
1 Klinman,D., Ishii,K. and Verthelyi,D.
  Oligodeoxynucleotide and its use to induce an immune response
  Patent: WO 0151500-A 101 19-JUL-2001;
  Secretary of the Department of Health and Human Services (US)
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Query Match          91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
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Db 3 TGCACCGGTGCAGGGGG 20

RESULT 15
AX352199
LOCUS AX352199 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 495 from Patent WO0193902.
ACCESSION AX352199
VERSION AX352199.1 GI:18617482
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
1 Mond,J.J., Flora,M. and Klinman,D.M.
  Immunostimulatory rna/dna hybrid molecules
  Patent: WO 0193902-A 495 13-DEC-2001;
  Biosynexus Incorporated (US)
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Query Match          91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
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Db 3 TGCACCGGTGCAGGGGG 20

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Job time : 636.732 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:09:30 ; Search time 28.2073 Seconds
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Title: US-10-068-160-13

Perfect score: 18

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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	14.8	82.2	1446	3	US-09-170-496D-207
C 4	14.8	82.2	1626	3	US-08-959-381A-4
C 5	14.8	82.2	3358	3	US-09-248-571-2
C 6	14.8	82.2	3358	4	US-09-553-736-2
C 7	14.8	82.2	24707	4	US-09-740-027-3
C 8	14.8	82.2	38653	4	US-09-922-445-1
C 9	14.4	80.0	265	4	US-09-313-294A-385
C 10	14.4	80.0	2194	4	US-09-021-655-668
C 11	14.4	80.0	2194	4	US-09-021-655-668
C 12	14.4	77.8	1350	4	US-09-252-991A-677
C 13	14.4	77.8	1350	4	US-08-840-316-4
C 14	14.4	77.8	7168	3	US-08-809-523-4
C 15	14.4	77.8	7168	3	US-08-471-971-4
C 16	14.4	77.8	7168	4	US-09-402-776-4
C 17	14.4	77.8	7168	5	PCT-US93-08849A-4
C 18	14.4	77.8	7168	5	PCT-US93-08849A-4
C 19	14.4	77.8	7195	3	US-08-478-507-6
C 20	14.4	77.8	7195	3	US-09-128-275A-6
C 21	14.4	77.8	7195	4	US-09-553-427-6
C 22	13.8	76.7	96	4	US-09-342-681C-107
C 23	13.8	76.7	106	1	US-08-441-591-18
C 24	13.8	76.7	106	1	US-08-441-591-19
C 25	13.8	76.7	106	1	US-08-303-362A-18
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C 27	13.8	76.7	106	5	PCT-US95-05600-35

28	13.8	76.7	106	5	PCT-US95-05600-36
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C 32	13.8	76.7	204	4	US-09-313-294A-7594
C 33	13.8	76.7	382	4	US-09-833-381-178
C 34	13.8	76.7	633	4	US-09-489-039A-2752
C 35	13.8	76.7	672	4	US-09-511-881A-1
C 36	13.8	76.7	672	4	US-09-511-881A-2
C 37	13.8	76.7	750	4	US-09-833-381-1453
C 38	13.8	76.7	885	4	US-09-252-991A-7532
C 39	13.8	76.7	899	4	US-09-171-209-50
C 40	13.8	76.7	912	4	US-09-252-991A-7811
C 41	13.8	76.7	1038	1	US-08-031-148-3
C 42	13.8	76.7	1038	3	US-08-415-838-3
C 43	13.8	76.7	1038	4	US-09-205-169-3
C 44	13.8	76.7	1242	4	US-09-252-991A-7949
C 45	13.8	76.7	1359	4	US-09-489-039A-2500

ALIGNMENTS

RESULT 1
US-08-959-381A-3/c
; Sequence 3, Application US/08959381A
; Patent No. 6048711
; GENERAL INFORMATION:
; APPLICANT: HINUMA, SHUJI
; APPLICANT: FUKUSUMI, SHOUJI
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; TITLE OF INVENTION: POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/959,381A
; FILING DATE: 28-OCT-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 286823/1996
; FILING DATE: 29-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: TAK-50003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1443 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-959-381A-3

Query Match 82.2% ; Score 14.8; DB 3; Length 1443;
Best Local Similarity 88.9% ; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 82.2%; Score 14.8; DB 3; Length 3358;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
||||| |||||||
Db 999 TGCACCATGCAGGGGG 1016

RESULT 6
US-09-553-736-2
; Sequence 2, Application US/09553736
; Patent No. 6440672
; GENERAL INFORMATION:
; APPLICANT: BASBAUM, Carol
; APPLICANT: GALLUP, Marianne
; APPLICANT: DAIJONG, Li
; APPLICANT: GEREMICHAEL, Assefa
; APPLICANT: GENSCH, Erin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE INHIBITION OF MUC-5
; TITLE OF INVENTION: MUCIN GENE EXPRESSION
; FILE REFERENCE: UCSF-013/0305
; CURRENT APPLICATION NUMBER: US/09/553,736
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 09/248,571
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: US 60/074,398
; PRIOR FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 3358
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-553-736-2

Query Match 82.2%; Score 14.8; DB 4; Length 3358;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
||||| |||||||
Db 999 TGCACCATGCAGGGGG 1016

RESULT 7
US-09-740-027-3
; Sequence 3, Application US/09740027
; Patent No. 6485939
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER COFACTOR
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER
; TITLE OF INVENTION: COFACTOR PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO01052
; CURRENT APPLICATION NUMBER: US/09/740,027
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 24707
; TYPE: DNA
; ORGANISM: Human
US-09-740-027-3

Query Match 82.2%; Score 14.8; DB 4; Length 24707;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
||||| |||||||
Db 17471 TGCACGGGGCAGGGAGG 17488

RESULT 8
US-09-922-445-1/c
; Sequence 1, Application US/09922445
; Patent No. 6528268
; GENERAL INFORMATION:
; APPLICANT: Andersson, Maria K.
; APPLICANT: Berglund, Lars G. T.
; APPLICANT: Reneland, Rikard H.
; APPLICANT: Adam, Gail I. R.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
; FILE REFERENCE: GGI26US
; CURRENT APPLICATION NUMBER: US/09/922,445
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 38653
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(26156)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (24801)..(24801)
; OTHER INFORMATION: nucleotide 24801 is a single nucleotide polymorphism which can be
; OTHER INFORMATION: A or G
; NAME/KEY: misc feature
; LOCATION: (24941)..(24941)
; OTHER INFORMATION: nucleotide 24941 is a single nucleotide polymorphism which can be
; OTHER INFORMATION: T or C
; NAME/KEY: exon
; LOCATION: (26157)..(26252)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (26253)..(26401)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (26402)..(26543)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (26544)..(27024)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (27025)..(27178)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (27179)..(30519)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (27645)..(27645)
; OTHER INFORMATION: nucleotide 27645 is a single nucleotide polymorphism which can be
; OTHER INFORMATION: C or G
; NAME/KEY: exon
; LOCATION: (30520)..(30681)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (30682)..(30894)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (30895)..(31027)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (31028)..(31747)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (31748)..(31841)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (31842)..(32400)
; OTHER INFORMATION:

NAME/KEY: misc feature
LOCATION: (32163)..
OTHER INFORMATION: nucleotide 32163 is a single nucleotide polymorphism which can be
NAME/KEY: exon
LOCATION: (32401)..
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (32529)..
OTHER INFORMATION:
NAME/KEY: misc feature
LOCATION: (32614)..
OTHER INFORMATION: nucleotide 32614 is a single nucleotide polymorphism which can be
NAME/KEY: exon
LOCATION: (33415)..
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (33598)..
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (34315)..
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (34589)..
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (36405)..
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (36524)..
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (38342)..
OTHER INFORMATION:
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank/AC004923
DATABASE ENTRY DATE: 1999-12-21
RELEVANT RESIDUES: (1)..
US-09-922-445-1

Query Match 82.2%; Score 14.8; DB 4; Length 38653;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
Db 14712 TGCACGTGGGCAGGGGG 14695

RESULT 9
US-09-313-294A-385
Sequence 385, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalagudi, Raghunath V.
APPLICANT: Ito, Laura I.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 385
LENGTH: 265
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700549120HI
NAME/KEY: unsure
LOCATION: 3, 7, 39, 240

OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-385
Query Match 80.0%; Score 14.4; DB 4; Length 265;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCACCGGTGCAGGGGG 17
Db 89 GCACCGGAGCAGGGGG 104

RESULT 10
US-09-023-655-668
Sequence 668, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 668:
SEQUENCE CHARACTERISTICS:
LENGTH: 2194 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BOSTHE02
CLONE: 409041
US-09-023-655-668

Query Match 80.0%; Score 14.4; DB 4; Length 2194;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCACCGGTGCAGGGGG 17
Db 2116 GCACCGGTTCAGGGGG 2131

RESULT 11
US-09-252-991A-736
Sequence 736, Application US/09252991A

```

; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 735
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-736

Query Match 77.8%; Score 14; DB 4; Length 732;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCACCGGTGCAGGG 15
Db 523 GCACCGGTGCAGGG 536

RESULT 12
US-09-252-991A-677/c
; Sequence 677, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 677
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-677

Query Match 77.8%; Score 14; DB 4; Length 1350;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCACCGGTGCAGGG 15
Db 678 GCACCGGTGCAGGG 665

RESULT 13
US-08-840-316-4/c
; Sequence 4, Application US/08840316
; Patent No. 6054567
; GENERAL INFORMATION:
; APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,
; APPLICANT: Tsarev, Sergei. A., and Robinson, Robin A.
; TITLE OF INVENTION: Recombinant Protein Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE

```

```

; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,316
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard W. Bork
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4255
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7168 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-840-316-4

Query Match 77.8%; Score 14; DB 3; Length 7168;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCGGTGCAGGGGG 18
Db 2263 CCGGTGCAGGGGG 2250

RESULT 14
US-08-809-523-4/c
; Sequence 4, Application US/08809523
; Patent No. 6207416
; GENERAL INFORMATION:
; APPLICANT: Tsarev, Sergei. A., Emerson,
; APPLICANT: Suzanne U., Purcell, Robert H.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,523
; FILING DATE: 28-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13102
; FILING DATE: 03-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/316,765
; FILING DATE: 03-OCT-1994

```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/947,263
; FILING DATE: 18-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard W. Bork
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4032US4
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7168 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-809-523-4

Query Match          77.8%; Score 14; DB 3; Length 7168;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CCGGTGCAGGGGGG 18
        |||||
DB      2263 CCGGTGCAGGGGGG 2250

Search completed: July 2, 2004, 13:37:23
Job time : 29.2073 secs

; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-471-971-4

Query Match          77.8%; Score 14; DB 3; Length 7168;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CCGGTGCAGGGGGG 18
        |||||
DB      2263 CCGGTGCAGGGGGG 2250

Search completed: July 2, 2004, 13:37:23
Job time : 29.2073 secs
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Sequence 496, Application US/09874991C
Publication No. US20040052763A1
GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: KLINMAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 507
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-507

Query Match 100.0%; Score 18; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGGG 18
|||
DB 3 TGCACCGGTGCAGGGGGG 20

RESULT 5
US-09-874-991C-514
Sequence 514, Application US/09874991C
Publication No. US20040052763A1
GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: KLINMAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 514
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-514

Query Match 100.0%; Score 18; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGGG 18
|||
DB 3 TGCACCGGTGCAGGGGGG 20

RESULT 6
US-09-874-991C-540
Sequence 540, Application US/09874991C
Publication No. US20040052763A1
GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: KLINMAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: PatentIn Ver. 2.1

Sequence 496, Application US/09874991C
Publication No. US20040052763A1
GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: KLINMAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 496
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-496

Query Match 100.0%; Score 18; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGGG 18
|||
DB 3 TGCACCGGTGCAGGGGGG 20

RESULT 3
US-09-874-991C-504
Sequence 504, Application US/09874991C
Publication No. US20040052763A1
GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: KLINMAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 504
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-504

Query Match 100.0%; Score 18; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGGG 18
|||
DB 3 TGCACCGGTGCAGGGGGG 20

RESULT 4
US-09-874-991C-507
Sequence 507, Application US/09874991C
Publication No. US20040052763A1
GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: KLINMAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES

```
; SEQ ID NO 540
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-540

Query Match      100.0%; Score 18; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
    |||||
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 7
US-10-068-160-2
; Sequence 2, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-2

Query Match      100.0%; Score 18; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
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Db 3 TGCACCGGTGCAGGGGG 20

RESULT 8
US-10-194-035-42
; Sequence 42, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-42

Query Match      100.0%; Score 18; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
    |||||
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 9
US-10-666-022-2
; Sequence 2, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Verthelyi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: misc feature
; LOCATION: (1)...(20)
; OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-2

Query Match      100.0%; Score 18; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
    |||||
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 10
US-10-666-022-178
; Sequence 178, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Verthelyi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 178
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-666-022-178

Query Match      100.0%; Score 18; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
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Db 3 TGCACCGGTGCAGGGGG 20

RESULT 13
US-09-874-991C-529
; Sequence 529, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 529
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-529

Query Match      100.0%; Score 18; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
   |||||
Db 11 TGCACCGGTGCAGGGGG 28

RESULT 14
US-09-874-991C-537
; Sequence 537, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 537
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-537

Query Match      100.0%; Score 18; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
   |||||
Db 11 TGCACCGGTGCAGGGGG 28

```

```

; SEQ ID NO 178
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-666-022-178

Query Match      100.0%; Score 18; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
   |||||
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 11
US-09-874-991C-517
; Sequence 517, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 517
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-517

Query Match      100.0%; Score 18; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
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Db 3 TGCACCGGTGCAGGGGG 20

RESULT 12
US-09-874-991C-525
; Sequence 525, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 525
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-525

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Db 11 TGCACCGGTGCAGGGGG 28

RESULT 15

US-09-874-991C-548
; Sequence 548, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 548
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-548

Query Match 100.0%; Score 18; DB 13; Length 40;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
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Db 16 TGCACCGGTGCAGGGGG 33

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Job time : 139.732 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:38:45 ; Search time 1348.02 Seconds
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Title: US-10-068-160-13
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

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Listing first 45 summaries

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2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
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22: em_gss_mam:*
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24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gsal:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	94.4	840	29	CG271799
C 2	16.4	91.1	245	10	AW325275
C 3	16.4	91.1	277	28	AQ444154
C 4	16.4	91.1	339	14	CB076094

C 5	16.4	91.1	440	14	CB087291
C 6	16.4	91.1	509	14	CB087214
C 7	16.4	91.1	562	9	AI370313
C 8	16.4	91.1	598	14	CB087325
C 9	16.4	91.1	610	29	CG892380
C 10	16.4	91.1	684	12	BMG24520
C 11	16.4	91.1	692	12	BMG20160
C 12	16.4	91.1	708	12	BMG21890
C 13	16.4	91.1	779	28	CG109078
C 14	16.4	91.1	799	28	CG133230
C 15	16.4	91.1	866	14	CK151795
C 16	16.4	91.1	1005	29	CNS04021
C 17	16.4	91.1	1120	28	CD214014
C 18	16.4	91.1	1200	14	CD256849
C 19	16	88.9	553	14	CB334319
C 20	16	88.9	700	12	BI897515
C 21	16	88.9	969	29	CNS03H3D
C 22	16	88.9	982	29	CNS042UH
C 23	16	88.9	1200	13	EX426076
C 24	16	88.9	1309	12	BM559504
C 25	15.4	85.6	105	14	CB486533
C 26	15.4	85.6	160	14	CB016628
C 27	15.4	85.6	220	29	CG222603
C 28	15.4	85.6	253	10	BE148995
C 29	15.4	85.6	274	9	AV108043
C 30	15.4	85.6	331	9	AI216300
C 31	15.4	85.6	331	13	BM268033
C 32	15.4	85.6	332	14	CB406325
C 33	15.4	85.6	344	28	AQ067086
C 34	15.4	85.6	375	13	BY315784
C 35	15.4	85.6	391	14	CD598131
C 36	15.4	85.6	397	29	CB437108
C 37	15.4	85.6	402	29	CE182406
C 38	15.4	85.6	405	12	BM487257
C 39	15.4	85.6	408	9	AI146003
C 40	15.4	85.6	411	10	BF386534
C 41	15.4	85.6	411	10	AW264336
C 42	15.4	85.6	418	12	BG381382
C 43	15.4	85.6	429	10	BP412974
C 44	15.4	85.6	450	9	AW024189
C 45	15.4	85.6	458	13	CA111141

ALIGNMENTS

RESULT 1
CG271799
LOCUS
DEFINITION
CG271799
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CG271799
OG0D226TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0596F04,
genomic survey sequence.
CG271799
CG271799.1 GI:34183940
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases i to 840)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Numborg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OG0D226TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP

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FEATURES
  source
    Class: sheared ends.
    Location/Qualifiers
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        /organism="Zea mays"
        /mol_type="genomic DNA"
        /strain="B73"
        /db_xref="taxon:4577"
        /clone="ZMBMa0696F04"
        /clone_lib="ZM 0.7 1.5 KB"
        /notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
        methylation filtered genomic DNA library"
ORIGIN
  Query Match          94.4%; Score 17; DB 29; Length 840;
  Best Local Similarity 100.0%; Pred. No. 6.3e+03;
  Mismatches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 2 GCACCGGTGCAGGGGG 18
  DB 502 GCACCGGTGCAGGGGG 518

RESULT 2
AW325275/c
LOCUS
DEFINITION
  TEN6637 T. cruzi epimastigote normalized cDNA library Trypanosoma
  cruzi cDNA clone 25h9 5', mRNA sequence.
ACCESSION
  AW325275
VERSION
  AW325275.1 GI:6761196
KEYWORDS
  EST.
SOURCE
  Trypanosoma cruzi
  ORGANISM
    Trypanosoma cruzi
    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
    Trypanosoma; Schizotrypanum.
REFERENCE
  1 (bases 1 to 245)
  Porcel, B.M., Tran, A.-N., Tammi, M., Nyarady, Z., Rydaker, M.,
  Urmenyi, T.P., Rondinelli, E., Pettersson, U., Andersson, B. and
  Aslund, L.
  Title: Gene survey of the pathogenic protozoan Trypanosoma cruzi
  Journal: Genome Res. 10 (8), 1103-1107 (2000)
  Medline: 20414748
  Pubmed: 10958628
  Comment:
    Contact: Aslund L
    Department of Medical Genetics
    Uppsala University
    Biomedical Center, Box 589, S-751 23 Uppsala, Sweden
    Tel: 46 18 471 45 85
    Fax: 46 18 52 68 49
    Email: lena.aslund@medgen.uu.se
    Seq primer: T7 primer
    High quality sequence stop: 245.
FEATURES
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    1..245
      /organism="Trypanosoma cruzi"
      /mol_type="mRNA"
      /strain="Cl-Brenner"
      /db_xref="taxon:5693"
      /clone="25h9"
      /cell_type="epimastigote"
      /clone_lib="T. cruzi epimastigote normalized cDNA Library"
      /notes="cDNA library constructed with oligo dt primed
      epimastigote mRNA and cloned in pT7c318D phagemid with
      modified polylinker (Pharmacia)"
ORIGIN
  Query Match          91.1%; Score 16.4; DB 10; Length 245;
  Best Local Similarity 94.4%; Pred. No. 1e+04;
  Mismatches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
  QY 1 TGCACCGGTGCAGGGGG 18
  DB 65 TGCATCGGTGCAGGGGG 48

FEATURES
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    Class: sheared ends.
    Location/Qualifiers
      1..840
        /organism="Zea mays"
        /mol_type="genomic DNA"
        /strain="B73"
        /db_xref="taxon:4577"
        /clone="ZMBMa0696F04"
        /clone_lib="ZM 0.7 1.5 KB"
        /notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
        methylation filtered genomic DNA library"
ORIGIN
  Query Match          94.4%; Score 17; DB 29; Length 840;
  Best Local Similarity 100.0%; Pred. No. 6.3e+03;
  Mismatches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 2 GCACCGGTGCAGGGGG 18
  DB 502 GCACCGGTGCAGGGGG 518

RESULT 3
AQ444154/c
LOCUS
DEFINITION
  GSSTc0207 Trypanosoma cruzi random genomic library Trypanosoma
  cruzi genomic clone Gl0L7, genomic survey sequence.
ACCESSION
  AQ444154
VERSION
  AQ444154.3 GI:10130745
KEYWORDS
  GSS.
SOURCE
  Trypanosoma cruzi
  ORGANISM
    Trypanosoma cruzi
    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
    Trypanosoma; Schizotrypanum.
REFERENCE
  1 (bases 1 to 277)
  Aguero, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.
  A random sequencing approach for the analysis of the trypanosoma
  cruzi genome: general structure, large gene and repetitive DNA
  families, and Gene discovery
  Genome Res. 10 (12), 1996-2005 (2000)
  Medline: 20568489
  Pubmed: 11116094
  Comment:
    On Sep 14, 2000 this sequence version replaced gi:9372108.
    Contact: Sanchez D.O.
    Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
    San Martin)
    Av. Gral. Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos
    Aires, Argentina
    Tel: (54-11) 4752-9639
    Fax: (54-11) 4752-9639
    Email: dsanchez@iib.unsam.edu.ar
    Sequences were basecalled with phred and vector was masked with
    crossmatch (see http://genome.washington.edu). Sequences were then
    trimmed from both ends to remove low quality bases and masked
    vector.
    Seq primer: T7
    Class: shotgun.
    Location/Qualifiers
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        /strain="Cl-Brenner"
        /db_xref="taxon:5693"
        /clone="Gl0L7"
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        /clone_lib="Trypanosoma cruzi random genomic library"
        /notes="Vector: pBS(-) (Stratagene); T. cruzi DNA was
        randomly sheared using a nebulizer and the 1 to 2 Kb range
        was gel purified and cloned into the dephosphoryated
        HincII site of the vector"
ORIGIN
  Query Match          91.1%; Score 16.4; DB 28; Length 277;
  Best Local Similarity 94.4%; Pred. No. 1e+04;
  Mismatches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
  QY 1 TGCACCGGTGCAGGGGG 18
  DB 238 TGCATCGGTGCAGGGGG 221

RESULT 4
CB076094/c
LOCUS
DEFINITION
  CB076094 Hedyotis terminalis flower - Stage 2 (NYBG) Hedyotis
  terminalis cDNA clone hf37c06, mRNA sequence.
ACCESSION
  CB076094
VERSION
  CB076094.1 GI:2789531
KEYWORDS
  EST.
SOURCE
  Hedyotis terminalis
  ORGANISM
    Hedyotis terminalis
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    asterids; lamids; Gentianales; Rubiaceae; Rubioideae;

```

```

REFERENCE
AUTHORS
1 (Bases 1 to 339)
Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P. and Stevenson,D.
Expressed tag sequences from Hedyotis terminalis flower - Stage 2
(NYBG)
JOURNAL
COMMENT
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: h337 row: c column: 06
Seq primer: -2LM13UnivRev
High quality sequence stop: 339.
Location/Qualifiers
1. .339
/organism="Hedyotis terminalis"
/mol_type="mRNA"
/db_xref="taxon:219667"
/dev_stage="pre-anthesis; Stage 2"
/clone_lib="Hedyotis terminalis flower - Stage 2 (NYBG)"
/site="Organ: flower; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts. Sample: collected on the island of
Hawaii, Hawaii; NYBG herbarium voucher TM2562"

ORIGIN
Query Match 91.1%; Score 16.4; DB 14; Length 339;
Best Local Similarity 94.4%; Pred. No. 1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
|||||
Db 97 TGCACCTGGTCAGGGGG 80

RESULT 5
CB087291/c
LOCUS
DEFINITION
440 bp mRNA linear EST 27-JAN-2003
centranthoides cDNA clone hj98g11, mRNA sequence.
ACCESSION
CB087291.1 GI:27911483
VERSION
EST.
KEYWORDS
Hedyotis centranthoides
Hedyotis centranthoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Gentianales; Rubiaceae; Rubioidae;
Spermacoeae; Hedyotis.
REFERENCE
AUTHORS
Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P. and Stevenson,D.
Expressed tag sequences from Hedyotis centranthoides flower - Stage
2 (NYBG)
JOURNAL
COMMENT
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: h337 row: c column: 11
Seq primer: -2LM13UnivRev
High quality sequence stop: 509.
Location/Qualifiers
1. .509
/organism="Hedyotis centranthoides"
/mol_type="mRNA"
/db_xref="taxon:219666"
/dev_stage="pre-anthesis; Stage 2"
/clone_lib="Hedyotis centranthoides flower - Stage 2
(NYBG)"
/site="Organ: flower; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts. Sample: collected on the island of
Hawaii, Hawaii; NYBG herbarium voucher TM2563"

FEATURES
source
High quality sequence stop: 440.
Location/Qualifiers
1. .440
/organism="Hedyotis centranthoides"
/mol_type="mRNA"
/db_xref="taxon:219666"
/clone="hj98g11"
/dev_stage="pre-anthesis; Stage 2"
/clone_lib="Hedyotis centranthoides flower - Stage 2
(NYBG)"
/site="Organ: flower; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts. Sample: collected on the island of
Hawaii, Hawaii; NYBG herbarium voucher TM2563"

ORIGIN
Query Match 91.1%; Score 16.4; DB 14; Length 440;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
|||||
Db 129 TGCACCTGGTCAGGGGG 112

RESULT 6
CB087214/c
LOCUS
DEFINITION
509 bp mRNA linear EST 27-JAN-2003
centranthoides cDNA clone hj97e04, mRNA sequence.
ACCESSION
CB087214.1 GI:27911406
VERSION
EST.
KEYWORDS
Hedyotis centranthoides
Hedyotis centranthoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Gentianales; Rubiaceae; Rubioidae;
Spermacoeae; Hedyotis.
REFERENCE
AUTHORS
Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P. and Stevenson,D.
Expressed tag sequences from Hedyotis centranthoides flower - Stage
2 (NYBG)
JOURNAL
COMMENT
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: hj97 row: e column: 04
Seq primer: -2LM13UnivRev
High quality sequence stop: 509.
Location/Qualifiers
1. .509
/organism="Hedyotis centranthoides"
/mol_type="mRNA"
/db_xref="taxon:219666"
/dev_stage="pre-anthesis; Stage 2"
/clone_lib="Hedyotis centranthoides flower - Stage 2
(NYBG)"
/site="Organ: flower; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts. Sample: collected on the island of
Hawaii, Hawaii; NYBG herbarium voucher TM2563"

FEATURES
source
High quality sequence stop: 440.
Location/Qualifiers
1. .440
/organism="Hedyotis centranthoides"
/mol_type="mRNA"
/db_xref="taxon:219666"
/clone="hj97e04"
/dev_stage="pre-anthesis; Stage 2"
/clone_lib="Hedyotis centranthoides flower - Stage 2
(NYBG)"
/site="Organ: flower; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts. Sample: collected on the island of
Hawaii, Hawaii; NYBG herbarium voucher TM2563"

```

EST.
Hedyotis centranthoides
Hedyotis centranthoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Gentianales; Rubiaceae; Rubioideae;
Spermacoceae; Hedyotis.
1 (bases 1 to 598)
Levesque, M.P., Twigg, R.W., Motley, T., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Ballja, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P. and Stevenson, D.
Expressed tag sequences from Hedyotis centranthoides flower - Stage
2 (NYBG)

UNPUBLISHED (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: hk03 row: f column: 05
Seq primer: -21M13UnivRev
High quality sequence stop: 598.
Location/Qualifiers
1..598
/organism="Hedyotis centranthoides"
/mol_type="mRNA"
/db_xref="taxon:219656"
/clones="hk03f05"
/dev_stage="pre-anthesis; Stage 2"
/clone_lib="Hedyotis centranthoides flower - Stage 2
(NYBG)"
/note="Organ: flower; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts. Sample: collected on the island of
Hawaii, Hawaii; NYBG herbarium voucher TM2563"

ORIGIN
Query Match 91.1%; Score 16.4; DB 14; Length 598;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
|||||
Db 146 TGCACCTGTCAGGGGG 129
|||||

RESULT 9
CG692380 610 bp DNA linear GSS 14-OCT-2003
LOCUS ZMMBB0292G11.f ZMMBB Zea mays subsp. mays genomic clone
DEFINITION ZMMBB0292G11 5', genomic survey sequence.
ACCESSION CG692380
VERSION CG692380.1 GI:37656062
KEYWORDS GSS.
SOURCE Zea mays subsp. mays (maize)
ORGANISM Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 610)
Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.
and Wing, R.
Sequencing of the maize genome
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA

ORIGIN
Query Match 91.1%; Score 16.4; DB 14; Length 509;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
|||||
Db 144 TGCACCTGTCAGGGGG 127
|||||

RESULT 7
AI370313 562 bp mRNA linear EST 15-FEB-1999
LOCUS qv76e01.x1 NCI CGAP Ut1 Homo sapiens cDNA clone IMAGE:1987512 3'
DEFINITION similar to TR:Q13045 Q13045 FLII 1, mRNA sequence.
ACCESSION AI370313
VERSION AI370313.1 GI:4149066
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 562)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1872 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 394.
Location/Qualifiers
1..562
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1987512"
/tissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host="DH103"
/clone_lib="NCI CGAP Ut1"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

ORIGIN
Query Match 91.1%; Score 16.4; DB 9; Length 562;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
|||||
Db 509 TGCACCGGTGCAGGGGG 526
|||||

RESULT 8
CB087525/c 598 bp mRNA linear EST 27-JAN-2003
LOCUS CB087525
DEFINITION hk03f05.g1 Hedyotis centranthoides flower - Stage 2 (NYBG) Hedyotis
centranthoides cDNA clone hk03f05, mRNA sequence.
ACCESSION CB087525
VERSION CB087525.1 GI:27911717

Tel: 520 626 3967
Fax: 520 621 9288
Email: <http://genome.arizona.edu>
PCR Primers:
FORWARD: T7
BACKWARD: M13r
Plate: 0292 row: G column: 11
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. 610
/organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
/cultivar="B73"
/sub_species="mays"
/db_xref="taxon:4578"
/clone="ZMWBB0292G11"
/lab_host="DH10B"
/clone_lib="ZMWBBb"
/note="Vector: pBelobAC11; Site 1: HindIII; Site 2: HindIII; Zea mays L. ssp. mays"

ORIGIN
Query Match 91.1%; Score 16.4; DB 29; Length 610;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
|||||
Db 525 TGCACCGGTTCAGGGGG 542

RESULT 10
BM624520/c
LOCUS BM624520 684 bp mRNA linear EST 26-FEB-2002
DEFINITION 17000687491457 A.Gam.ad.cdNA1 Anopheles gambiae cDNA clone
ACCESSION BM624520
VERSION 19600449632784 5', mRNA sequence.
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
REFERENCE 1 (bases 1 to 684)
AUTHORS Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
TITLE Celera Anopheles gambiae EST project
JOURNAL Unpublished (2002)
COMMENT Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRA@celera.com
Plate: NU01004ABX row: 1 column: 06
Seq primer: M13 Reverse.
Location/Qualifiers
1. 684
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
/db_xref="taxon:7165"
/clone="19600449632784"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="A.Gam.ad.cdNA1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."

FEATURES
source
1. 684

ORIGIN
Query Match 91.1%; Score 16.4; DB 12; Length 692;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
|||||
Db 183 TGCACCGGTGCAGGGGG 166

RESULT 12
BM621890/c
LOCUS BM621890 708 bp mRNA linear EST 25-FEB-2002
DEFINITION 17000687447901 A.Gam.ad.cdNA1 Anopheles gambiae cDNA clone
ACCESSION 19600449620865 5', mRNA sequence.
BM621890

ORIGIN
Query Match 91.1%; Score 16.4; DB 12; Length 692;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
|||||
Db 183 TGCACCGGTGCAGGGGG 166

RESULT 12
BM621890/c
LOCUS BM621890 708 bp mRNA linear EST 25-FEB-2002
DEFINITION 17000687447901 A.Gam.ad.cdNA1 Anopheles gambiae cDNA clone
ACCESSION 19600449620865 5', mRNA sequence.
BM621890

VERSION BM621890.1 GI:18920308
 EST.
 KEYWORDS Anopheles gambiae (African malaria mosquito)
 SOURCE Anopheles gambiae
 ORGANISM Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 1 (bases 1 to 708)
 REFERENCE Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L. Celerera Anopheles gambiae EST project Unpublished (2002)
 JOURNAL Contact: Holt R.A.
 COMMENT Celerera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltRA@celera.com
 Plate: NU01004NBU row: H column: 15
 Seq primer: M13 Reverse.
 Location/Qualifiers
 1..708
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449620865"
 /dev_stage="Adult"
 /lab_host="DH10b"
 /clone_lib="A.Gam.ad.cDNA1"
 /notes="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
 ORIGIN
 Query Match 91.1%; Score 16.4; DB 12; Length 708;
 Best Local Similarity 94.4%; Pred. No. 1.1e+04;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCACCGTGCACGGGGG 18
 Db 153 TGCACCGTGCACGGGGG 136
 RESULT 13
 LOCUS CCI09078 779 bp DNA linear GSS 16-APR-2003
 DEFINITION NDL.50B23.T7 Notre Dame Liverpool Aedes aegypti genomic clone
 ACCESSION CCI09078
 VERSION CCI09078.1 GI:29978133
 KEYWORDS GSS.
 SOURCE Aedes aegypti (yellow fever mosquito)
 ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes; Stegomyia.
 REFERENCE Loftus, B., Shetty, J., Knudson, D. and Severson, D. BAC end sequencing of Aedes aegypti Unpublished (2003)
 JOURNAL Other_GSSs: NDL.50B23.SP6
 COMMENT Contact: Brendan Loftus
 Department of Eukaryotic Genomics
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: enta@tigr.org
 Library was provided by David Severson
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers
 1..799
 /organism="Aedes aegypti"
 /mol_type="genomic DNA"
 /strain="liverpool"
 /db_xref="taxon:7159"
 /clone="NDL.50B23"
 /note="Vector: pECBAC1; Site 1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"

Library was provided by David Severson
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers
 1..779
 /organism="Aedes aegypti"
 /mol_type="genomic DNA"
 /strain="liverpool"
 /db_xref="taxon:7159"
 /clone="NDL.50B23"
 /note="Vector: pECBAC1; Site 1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"

FEATURES source
 ORIGIN
 Query Match 91.1%; Score 16.4; DB 28; Length 779;
 Best Local Similarity 94.4%; Pred. No. 1.1e+04;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCACCGTGCACGGGGG 18
 Db 306 TGCACCGTGCACGGGGG 289
 RESULT 14
 LOCUS CCI33230 799 bp DNA linear GSS 16-APR-2003
 DEFINITION NDL.50B22.T7 Notre Dame Liverpool Aedes aegypti genomic clone
 ACCESSION CCI33230
 VERSION CCI33230.1 GI:30002285
 KEYWORDS GSS.
 SOURCE Aedes aegypti (yellow fever mosquito)
 ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes; Stegomyia.
 REFERENCE Loftus, B., Shetty, J., Knudson, D. and Severson, D. BAC end sequencing of Aedes aegypti Unpublished (2003)
 JOURNAL Other_GSSs: NDL.50B22.SP6
 COMMENT Contact: Brendan Loftus
 Department of Eukaryotic Genomics
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: enta@tigr.org
 Library was provided by David Severson
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers
 1..799
 /organism="Aedes aegypti"
 /mol_type="genomic DNA"
 /strain="liverpool"
 /db_xref="taxon:7159"
 /clone="NDL.50B22"
 /note="Vector: pECBAC1; Site 1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"

FEATURES source
 ORIGIN
 Query Match 91.1%; Score 16.4; DB 28; Length 799;
 Best Local Similarity 94.4%; Pred. No. 1.1e+04;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCACCGTGCACGGGGG 18

RESULT 15
CK151795/c
LOCUS
DEFINITION FGAS034520 Triticum aestivum FGAS: Talt3 Triticum aestivum cDNA,
mRNA sequence.

ACCESSION CK151795
VERSION CK151795
KEYWORDS
SOURCE CK151795.1 GI:38970179

ORGANISM
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.

REFERENCE
AUTHORS Allard,F., Crosby,W.L., Danyluk,J., Budes,F., Frick,M., Gaudet,D.,
Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A.,
Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilsson,D.,
Penniket,C., Roach,J.L. and Sarhan,F.

TITLE Functional Genomics of Abiotic Stress In Wheat and Canola Crops
JOURNAL
COMMENT Unpublished (2003)

CONTACT: Mm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_estecs.usask.ca

FEATURES
source
1..866
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Wheat line CI 14106"
/db_xref="taxon:4565"
/lab_host="DHS alpha"
/clone_lib="Triticum aestivum FGAS: Talt3"
/note="Organ: Crown; Vector: pGEM-T; SSH (suppression
subtractive hybridization) cDNA library from genotype
CI14106 cold hardened at 2 C for 21 days and 49 days
(equal amount of cDNA pooled together before subtraction,
tester) and subtracted against genotype Norstar cold
hardened at 2 C for 1 day (24 h)(driver). Nitro-pyrole
anchored oligo-dt priming and non-directional cloning."

Plate: Talt328, row: K, column: 02.
Location/Qualifiers
1..866

ORIGIN
Query Match 91.1%; Score 16.4; DB 14; Length 866;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
DB 780 TGCACCGGTACAGGGGG 763

Search completed: July 2, 2004, 13:32:56
JOB time : 1351.14 secs

OM nucleic - nucleic search, using sw model
Run on: July 2, 2004, 07:36:05 ; Search time 563.317 Seconds
(without alignments)
1231.080 Million cell updates/sec

Title: US-10-068-160-15
Perfect score: 16
Sequence: 1 gggcatgcattgggggg 16
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenExbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.ma.*
20: em.om.*
21: em.ov.*
22: em.pat.*
23: em.ph.*
24: em.pl.*
25: em.ro.*
26: em.sts.*
27: em.un.*
28: em.vi.*
29: em.vi.*
30: em.htg.hum.*
31: em.htg.inv.*
32: em.htg.other.*
33: em.htg.mus.*
34: em.htg.pln.*
35: em.htg.rtd.*
36: em.htg.mam.*
37: em.htg.vrt.*
38: em.sy.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	16	100.0	55655	2	AC120183 Mus muscu
C 2	16	100.0	149773	2	AC118209 Mus muscu
C 3	16	100.0	154143	2	AC131924 Mus muscu
C 4	16	100.0	157263	2	AY178791 Canis fam
C 5	16	100.0	158920	2	AC135955 Canis fam
C 6	16	100.0	155077	10	AC084382 Mus muscu
C 7	16	100.0	183540	2	AC139123 Canis fam
C 8	16	100.0	186129	2	AC131987 Mus muscu
C 9	16	100.0	192462	9	CNS01RHC Human chr
C 10	16	100.0	222510	2	AC123656 Mus muscu
C 11	16	100.0	227805	2	AC147160 Mus muscu
C 12	16	100.0	234548	2	AC095635 Rattus no
C 13	16	100.0	345420	2	AC131337 Mus muscu
C 14	15	93.8	657	6	AX251652 Sequence
C 15	15	93.8	867	11	EV013263 S212P8739
C 16	15	93.8	2000	6	AX656277 Sequence
C 17	15	93.8	2808	8	ITU51741 Ipomoea tri
C 18	15	93.8	3387	8	AF032369 Cochliobo
C 19	15	93.8	3504	8	AF032368 Cochliobo
C 20	15	93.8	4349	8	NSETSPR X76056 N. sylvestr
C 21	15	93.8	5272	8	BSMAT2GEN X95814 B. sacchari
C 22	15	93.8	17687	1	AE001038 Archaeogl
C 23	15	93.8	64168	2	AC079003 Homo sapi
C 24	15	93.8	95280	9	AC073133 Homo sapi
C 25	15	93.8	107947	8	NCB7N14 AL669986 Neurospor
C 26	15	93.8	108645	9	AL359538 Human DNA
C 27	15	93.8	112416	2	AP000482 Homo sapi
C 28	15	93.8	117263	2	AC145324 Oryza sat
C 29	15	93.8	120832	9	AP001068 Homo sapi
C 30	15	93.8	121590	9	HS314N7 AL773602 Homo sapi
C 31	15	93.8	132875	9	AC112907 Homo sapi
C 32	15	93.8	132998	8	OSJN00098 AL606658 Oryza sat
C 33	15	93.8	145739	8	OSJN00157 AL662957 Oryza sat
C 34	15	93.8	148845	9	AP001067 Homo sapi
C 35	15	93.8	150889	9	AC106881 Homo sapi
C 36	15	93.8	155430	9	AL136160 Human DNA
C 37	15	93.8	157263	2	AY178791 Canis fam
C 38	15	93.8	157347	2	AP001882 Homo sapi
C 39	15	93.8	164725	9	AC092938 Homo sapi
C 40	15	93.8	168064	2	AC019160 Homo sapi
C 41	15	93.8	175550	2	AC009863 Homo sapi
C 42	15	93.8	175837	2	AC022045 Homo sapi
C 43	15	93.8	176155	2	AC012149 Homo sapi
C 44	15	93.8	177417	2	AC133160 Mus muscu
C 45	15	93.8	178975	2	AC023222 Homo sapi

ALIGNMENTS

RESULT 1
AC120183/c
LOCUS Mus musculus clone RP24-116K23, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC120183
ACCESSION AC120183
VERSION AC120183.1 GI:20429532
KEYWORDS HTG; HTGS PHASED.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 65655)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Mus musculus, clone RP24-116K23
JOURNAL Unpublished

AC120183 65655 bp DNA linear HTG 03-MAY-2002
Mus musculus clone RP24-116K23, LOW-PASS SEQUENCE SAMPLING.

REFERENCE
AUTHORS

2 (bases 1 to 65655)
 Birren, B., Linton, J., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
 Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,
 Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
 Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
 Cook, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J. S., Dodge, S.,
 Fero, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
 Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
 Kamat, A., Karatas, A., Kells, C., Lakocue, K., Lamazares, R.,
 Landers, T., Lehotzky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
 MacLean, C., Macdonald, P., Major, J., Margulis, N., Matthews, C.,
 McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneses, L.,
 Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
 Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D.,
 Oliver, J., Peterson, K., Phukhang, P., Pierre, N., Pollara, V.,
 Raymond, C., Retta, R., Ribback, M., Riley, R., Rise, C., Rogov, P.,
 Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,
 Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
 Topham, K., Travers, M., Travis, N., Triglio, J., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (03-MAY-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A. P. A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L25878
 Center clone name: 116_K_23

TITLE
JOURNAL
COMMENT

9715 10423: contig of 709 bp in length
 10424 10523: gap of 100 bp
 10524 12443: contig of 720 bp in length
 12443 13443: gap of 100 bp
 13443 12070: contig of 727 bp in length
 12070 12170: gap of 100 bp
 12170 12896: contig of 726 bp in length
 12896 12996: gap of 100 bp
 12996 13706: contig of 710 bp in length
 13706 13806: gap of 100 bp
 13806 14497: contig of 691 bp in length
 14497 14597: gap of 100 bp
 14597 15319: contig of 722 bp in length
 15319 16145: contig of 726 bp in length
 16145 16245: gap of 100 bp
 16245 16380: contig of 735 bp in length
 16380 17080: gap of 100 bp
 17080 17801: contig of 721 bp in length
 17801 17901: gap of 100 bp
 17901 18621: contig of 720 bp in length
 18621 18721: gap of 100 bp
 18721 19440: contig of 719 bp in length
 19440 19540: gap of 100 bp
 19540 20267: contig of 727 bp in length
 20267 20367: gap of 100 bp
 20367 21087: contig of 720 bp in length
 21087 21187: gap of 100 bp
 21187 21906: contig of 719 bp in length
 21906 22006: gap of 100 bp
 22006 22501: contig of 495 bp in length
 22501 22601: gap of 100 bp
 22601 23317: contig of 716 bp in length
 23317 23417: gap of 100 bp
 23417 24110: contig of 693 bp in length
 24110 24210: gap of 100 bp
 24210 24911: contig of 701 bp in length
 24911 25011: gap of 100 bp
 25011 25730: contig of 719 bp in length
 25730 25830: gap of 100 bp
 25830 26514: contig of 684 bp in length
 26514 26614: gap of 100 bp
 26614 27335: contig of 721 bp in length
 27335 27435: gap of 100 bp
 27435 28165: contig of 730 bp in length
 28165 28265: gap of 100 bp
 28265 28983: contig of 718 bp in length
 28983 29084: gap of 100 bp
 29084 29790: contig of 706 bp in length
 29790 29889: gap of 100 bp
 29889 30598: contig of 709 bp in length
 30598 30698: gap of 100 bp
 30698 31404: contig of 706 bp in length
 31404 31504: gap of 100 bp
 31504 32228: contig of 724 bp in length
 32228 32328: gap of 100 bp
 32328 33043: contig of 715 bp in length
 33043 33143: gap of 100 bp
 33143 33865: contig of 722 bp in length
 33865 33965: gap of 100 bp
 33965 34673: contig of 708 bp in length
 34673 34773: gap of 100 bp
 34773 35501: contig of 728 bp in length
 35501 35601: gap of 100 bp
 35601 36322: contig of 721 bp in length
 36322 36422: gap of 100 bp
 36422 37138: contig of 716 bp in length
 37138 37238: gap of 100 bp
 37238 37968: contig of 730 bp in length
 37968 38068: gap of 100 bp
 38068 38788: contig of 720 bp in length
 38788 38888: gap of 100 bp
 38888 39604: contig of 716 bp in length

* NOTE: This record contains 81 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

1 710: contig of 710 bp in length
 811 810: gap of 100 bp
 811 1525: contig of 715 bp in length
 1525 1625: gap of 100 bp
 1625 2347: contig of 722 bp in length
 2347 2447: gap of 100 bp
 2447 3154: contig of 707 bp in length
 3154 3254: gap of 100 bp
 3254 3949: contig of 695 bp in length
 3949 4049: gap of 100 bp
 4049 4768: contig of 719 bp in length
 4768 4868: gap of 100 bp
 4868 5594: contig of 726 bp in length
 5594 5694: gap of 100 bp
 5694 6378: contig of 684 bp in length
 6378 6478: gap of 100 bp
 6478 7188: contig of 710 bp in length
 7188 7288: gap of 100 bp
 7288 8003: contig of 715 bp in length
 8003 8103: gap of 100 bp
 8103 8805: contig of 702 bp in length
 8805 8905: gap of 100 bp
 8905 9614: contig of 709 bp in length
 9614 9714: gap of 100 bp

39704: gap of 100 bp
39705: contig of 719 bp in length
40423: gap of 100 bp
40523: gap of 729 bp in length
41252: contig of 100 bp
41352: gap of 716 bp in length
42069: gap of 100 bp
42168: gap of 720 bp in length
42888: contig of 100 bp
42989: gap of 714 bp in length
43702: gap of 100 bp
43802: gap of 737 bp in length
44539: gap of 100 bp
44639: gap of 726 bp in length
45365: gap of 100 bp
45465: gap of 726 bp in length
46191: contig of 100 bp
46291: gap of 100 bp
46984: contig of 593 bp in length
47800: gap of 100 bp
47800: contig of 716 bp in length
47900: gap of 100 bp
48615: gap of 715 bp in length
48715: gap of 100 bp
49305: contig of 590 bp in length
49405: gap of 100 bp
50119: contig of 714 bp in length
50219: gap of 100 bp
50932: contig of 713 bp in length
51032: gap of 100 bp
51766: contig of 734 bp in length
51866: gap of 100 bp
51967: contig of 718 bp in length
52584: gap of 100 bp
52684: gap of 708 bp in length
53392: contig of 708 bp in length
53492: gap of 100 bp
54209: contig of 717 bp in length
54309: gap of 100 bp
55026: contig of 717 bp in length
55136: gap of 100 bp
55834: contig of 708 bp in length
55934: gap of 100 bp

Query Match 100.0%; Score 16; DB 2; Length 65655;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGCGGGGGG 16
DB 29249 GGGCATGCGGGGGG 29234

AC118209 149773 bp DNA linear HTG 22-MAR-2003
Mus musculus clone RP24-566J22, WORKING DRAFT SEQUENCE, 6 unordered pieces.

AC118209
AC118209.3 GI:29150444
HTG: HTGS PHASE1; HTGS DRAFT.
MUS musculus (house mouse)

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP24-566J22
Unpublished
2 (bases 1 to 149773)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Collangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,

Farro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Larocque, K., Lamazares, R.,
Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G.,
Maclean, C., Macdonald, P., Major, J., Marguis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Menes, L.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (14-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 149773)

Birren, B., Nusbaum, C., Lander, E., Abouelheil, A., Allen, N.,
Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Faro, S.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Farro, S.,
Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C.,
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Meldrum, J., Menes, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (22-MAR-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 22, 2003 this sequence version replaced gi:24850514.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
Center project name: L21328
Center clone name: 566_J_22

----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 14886 bases at least Q40
Consensus quality: 149124 bases at least Q30
Consensus quality: 149185 bases at least Q20
Insert size: 151000; agarose-ff
Quality coverage: 149273; sum-of-contigs
Quality coverage: 12.5 in Q20 bases; agarose-ff
Quality coverage: 12.7 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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1 27796: contig of 27796 bp in length
27797 27896: gap of 100 bp
27897 33321: contig of 5425 bp in length
33322 33421: gap of 100 bp
33422 45908: contig of 12487 bp in length
45909 46008: gap of 100 bp
46009 85245: contig of 39237 bp in length
85246 85346: gap of 100 bp
85346 130509: contig of 45164 bp in length
130510 130609: gap of 100 bp
130610 149773: contig of 19164 bp in length.

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FEATURES

Source

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1. 149773
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP24-566J22"
/clone_lib="RPCI-24 Male Mouse BAC"

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misc_feature

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1. 27796
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clone_end:SP6
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27897..33321
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misc_feature

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misc_feature

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46009..85245
/note="assembly_fragment"

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misc_feature

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85346..130509
/note="assembly_fragment"

```

misc_feature

```

130610..149773
/note="assembly_fragment"
clone_end:T7
vector_side:right

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ORIGIN

Query Match 100.0%; Score 16; DB 2; Length 149773;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCATGCGGGGG 16

Db 91261 GGGCATGCGGGGG 91246

RESULT 3

AC131924

LOCUS AC131924 154143 bp DNA linear HTG 12-MAR-2003
 DEFINITION Mus musculus clone RP24-227A11, WORKING DRAFT SEQUENCE, 9 unordered
 pieces.

ACCESSION

AC131924.3 GI:28927740

VERSION

HTG; HTGS PHASE1; HTGS DRAFT.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 154143)

Birren, B., Nusbaum, C. and Lander, E.

Mus musculus, clone RP24-227A11

AUTHORS

Unpublished

JOURNAL

2 (bases 1 to 154143)

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,

Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,

Camarata, J., Chang, J., Chazaro, B., Choepel, J., Collymore, A.,

Cook, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J.S., Dodge, S.,

Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,

Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,

Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,

Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,

Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,
 McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
 Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
 O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
 Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
 Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P.,
 Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
 Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
 Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (27-AUG-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 154143)

REFERENCE

AUTHORS

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
 Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
 Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
 Collymore, A., Cook, A., Cooke, P., Corum, B., DeArelano, K.,
 Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
 Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S.,
 Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
 Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
 Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
 Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
 Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
 Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
 Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
 O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
 Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
 Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P.,
 Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
 Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M.,
 Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
 Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

COMMENT

Direct Submission

Submitted (12-MAR-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

On Mar 12, 2003 this sequence version replaced gi:28416184.

All repeats were identified using RepeatMasker:

Smit, A.P.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www.seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L27131

Center clone name: 227_A11

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 151397 bases at least Q40

Consensus quality: 152158 bases at least Q30

Consensus quality: 152629 bases at least Q20

Insert size: 155000; agarose-EP

Insert size: 153343; sum-of-contigs

Quality coverage: 10.5 in Q20 bases; agarose-fp

Quality coverage: 10.7 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 9 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 560: contig of 560 bp in length

* 561 660: gap of 100 bp

* 661 2921: contig of 2261 bp in length

* 2922 3021: gap of 100 bp

```

* 3022 10861: contig of 7840 bp in length
* 10862 10961: gap of 100 bp
* 21761 21762: contig of 10755 bp in length
* 21717 21816: gap of 100 bp
* 34324 34325: contig of 12508 bp in length
* 34325 34424: gap of 100 bp
* 34425 46524: contig of 12100 bp in length
* 46525 46624: gap of 100 bp
* 70365 70366: contig of 23740 bp in length
* 100316 100317: contig of 29852 bp in length
* 100317 100416: gap of 100 bp
* 100417 154143: contig of 53727 bp in length.

```

FEATURES

Location/Qualifiers

```

1..154143
  /organism="Mus musculus"
  /mol_type="genomic DNA"
  /db_xref="taxon:10090"
  /clone="RP24-227A11"
  /clone_lib="RPCI-24 Male Mouse BAC"
misc_feature
1..560
  /note="assembly_fragment"
  clone_end:SP6
  vector_side:left"
misc_feature
661..72921
  /note="assembly_fragment"
misc_feature
3022..10861
  /note="assembly_fragment"
misc_feature
10962..21716
  /note="assembly_fragment"
misc_feature
21817..34324
  /note="assembly_fragment"
misc_feature
34425..46524
  /note="assembly_fragment"
misc_feature
46625..70364
  /note="assembly_fragment"
misc_feature
70465..100316
  /note="assembly_fragment"
misc_feature
100417..154143
  /note="assembly_fragment"
  clone_end:T7
  vector_side:right"

```

ORIGIN

```

Query Match      100.0%; Score 16; DB 2; Length 154143;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GGGCAGTCATGGCGG 16
Db      66741 GGGCAGTCATGGCGG 66756

```

RESULT 4

```

AY178791
LOCUS      AY178791      157263 bp      DNA      linear      HTG 12-MAR-2003
DEFINITION Canis familiaris chromosome CFA9, *** SEQUENCING IN PROGRESS ***,
55 unordered pieces.
ACCESSION      AY178791.1 GI:25990197
VERSION      HTG; HTGS PHASE1.
KEYWORDS      Canis familiaris (dog)
SOURCE      Canis familiaris
ORGANISM      Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE      1 (bases 1 to 157263)
AUTHORS      Sidjanin,D.J., Miller,B., Kijas,J., McElwee,J., Pillardy,J.,
Malek,J., Pai,G., Feldblyum,T., Fraser,C., Acland,G. and Aguirre,G.
TITLE      Radiation hybrid map, physical map, and low-pass genomic sequence
of the canine pred region on CFA9 and comparative mapping with the
synetic region on human chromosome 17
JOURNAL      Genomics 81 (2), 138-148 (2003)
MEDLINE      22508185

```

PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

12620391
2 (bases 1 to 157263)
Sidjanin,D.J., Miller,B., Kijas,J., McElwee,J., Pillardy,J.,
Malek,J., Pai,G., Feldblyum,T., Fraser,C., Acland,G. and Aguirre,G.
Direct Submission
Submitted (14-NOV-2002) James A. Baker Institute for Animal Health,
Cornell University, Hungerford Hill Rd., Ithaca, NY 14853, USA
* NOTE: This is a 'working draft' sequence. It currently
* consists of 55 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
954 1053: contig of 953 bp in length
1054 1053: gap of unknown length
1054 2019: contig of 966 bp in length
2020 2119: gap of unknown length
2120 2119: contig of 1114 bp in length
2120 3233: gap of unknown length
3234 3233: contig of 955 bp in length
3234 4288: gap of unknown length
4289 4388: gap of unknown length
4389 5712: contig of 1324 bp in length
5713 5812: gap of unknown length
5813 5807: contig of 995 bp in length
5808 6907: gap of unknown length
6908 8116: contig of 1209 bp in length
8117 8216: gap of unknown length
8217 9050: contig of 834 bp in length
9051 9151: gap of unknown length
9151 10098: contig of 948 bp in length
10099 10198: gap of unknown length
10199 11341: contig of 1143 bp in length
11342 11341: gap of unknown length
11342 12317: contig of 875 bp in length
12317 12416: gap of unknown length
12417 13578: contig of 1162 bp in length
13579 13678: gap of unknown length
13679 14986: contig of 1308 bp in length
14987 15086: gap of unknown length
15087 15087: contig of 1388 bp in length
15087 16475: gap of unknown length
16475 16475: gap of unknown length
16475 17437: contig of 863 bp in length
17438 17537: gap of unknown length
17538 18264: contig of 1727 bp in length
18265 19364: gap of unknown length
19365 21032: contig of 1668 bp in length
21033 21132: gap of unknown length
21133 22044: contig of 912 bp in length
22045 22144: gap of unknown length
22145 23953: contig of 1809 bp in length
23954 24053: gap of unknown length
24054 24784: contig of 731 bp in length
24785 24884: gap of unknown length
24885 25808: contig of 924 bp in length
25809 25909: gap of unknown length
25909 27662: contig of 1754 bp in length
27663 29363: contig of 1601 bp in length
29364 29464: gap of unknown length
29464 30704: contig of 1241 bp in length
30705 31655: contig of 851 bp in length
31656 31756: gap of unknown length
31756 34159: contig of 2404 bp in length
34160 34259: gap of unknown length
34260 36278: contig of 2019 bp in length
36279 36378: gap of unknown length
36379 38287: contig of 1909 bp in length
38288 38388: gap of unknown length
38388 40069: contig of 1682 bp in length
40070 40169: gap of unknown length

```

40170 42358: contig of 2189 bp in length
* 42359: gap of unknown length
* 42360: contig of 1737 bp in length
44195: contig of unknown length
44296: gap of unknown length
44777: contig of 3182 bp in length
47577: gap of unknown length
49430: contig of 1853 bp in length
49530: gap of unknown length
52362: contig of 2832 bp in length
52462: gap of unknown length
52524: contig of 2792 bp in length
55354: gap of unknown length
55355: contig of 3713 bp in length
59067: gap of unknown length
59167: contig of 2811 bp in length
59168: gap of unknown length
61979: contig of 2991 bp in length
62079: contig of 1027 bp in length
65070: gap of unknown length
66196: contig of 3998 bp in length
66296: gap of unknown length
70294: contig of 3440 bp in length
70394: gap of unknown length
73334: gap of 3067 bp in length
73934: gap of unknown length
77001: contig of 3413 bp in length
77101: gap of unknown length
80514: contig of 3549 bp in length
80614: gap of unknown length
84163: contig of 3812 bp in length
84263: gap of unknown length
88075: gap of 4436 bp in length
88175: contig of 4786 bp in length
92611: gap of unknown length
92711: contig of 3553 bp in length
97498: gap of unknown length
97597: gap of unknown length
101150: contig of 5428 bp in length
101250: gap of unknown length
106578: contig of 7355 bp in length
106779: gap of unknown length
114133: contig of 7121 bp in length
114233: gap of unknown length
121354: contig of 6552 bp in length
121454: gap of unknown length
128107: contig of 8619 bp in length
128206: gap of unknown length
136825: contig of 8435 bp in length
136925: gap of unknown length
145360: contig of 11803 bp in length
145361: gap of unknown length
145461: 157263: contig of 11803 bp in length.

FEATURES
source
1..157263
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
/chromosome="CFA9"

ORIGIN
Query Match 100.0%; Score 16; DB 2; Length 157263;
Best Local Similarity 100.0%; Pred. NC. 11e-02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GGGCATGCGTGGGGG 16
31156 GGGCATGCGTGGGGG 31171

RESULT 5
AC135955 158920 bp DNA linear HTG 14-NOV-2002
LOCUS
DEFINITION
Canis familiaris clone RP81-65H2, WORKING DRAFT SEQUENCE, 3 ordered
pieces.

AC135955
AC135955.2 GI:24960942
HTG; HTGS PHASE2; HTGS DRAFT.
Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 158920)
Akher.N., Antonellis.A., Ayele.K., Beckstrom-Sternberg.S.M.,
Benjamin.B., Blakesley.N.W., Bouffard.G.G., Brinkley.C., Brooks.S.,
Carriaga.K., Coleman.B., Engle.J., Granite.S., Guan.X., Gupta.J.,
Haghighi.P., Han.J., Hansen.N., Ho.S.-L., Idol.J.R., Karling.E.,
Laric.P., Lee-Lin.S.-Q., Legaspi.R., Maduro.Q.L., Maduro.V.B.,
Margulies.E.H., Masiello.C., Maskeri.B., McDowell.J.,
Paquirigan.C., Pearson.R., Portnoy.M.E., Prasad.A.,
Reddix-Dugue.N., Schandler.K., Schueler.M.G., Sison.C.,
Stantrypop.S., Thomas.J.W., Thomas.P.J., Touchman.J.W., Vogt.J.L.,
Wetherby.K.D., Wiggins.D., Young.A. and Green.E.D.
NISC Comparative Sequencing Initiative
Unpublished
Green.E.D.
Direct Submission
Submitted (25-OCT-2002) NIH Intramural Sequencing Center, 8717
Grovermont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 158920)
Green.E.D.
Direct Submission
Submitted (14-NOV-2002) NIH Intramural Sequencing Center, 8717
Grovermont Circle, Gaithersburg, MD 20877, USA
On Nov 14, 2002 this sequence version replaced gi:24371373.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.zoo@nhgri.nih.gov
----- Project Information
Center project name: Cwu
Center clone name: 065H02

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 158022 bases at least Q40
Consensus quality: 158465 bases at least Q30
Consensus quality: 158648 bases at least Q20
Insert size: 138000; agarose-fp
Insert size: 138720; sum-of-contigs
Quality coverage: 11.42x in Q20 bases; agarose-fp
Quality coverage: 9.93x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

* 1 37538: contig of 37538 bp in length
* 37539 37638: gap of unknown length
* 37639 136759: contig of 99121 bp in length
* 136760 136859: gap of unknown length
* 136860 158920: contig of 22061 bp in length.

```

FEATURES

```

source
1..158920
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
/clone="RP81-65H2"
/clone_lib="RP81"

misc_feature
1..37538
/note="assembly_fragment"
clone_end:SP6
vector_side:left"

misc_feature
37639..136759
/note="assembly_fragment"

misc_feature
136860..158920
/note="assembly_fragment"
clone_end:T7
vector_side:right"

```

ORIGIN

```

Query Match 100.0%; Score 16; DB 2; Length 158920;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GGGCATGCGGGGGG 16
|||||

```

```

Db 20177 GGGCATGCGGGGGG 20192
|||||

```

RESULT 6

```

AC084382 AC084382 165077 bp DNA linear ROD 21-JUN-2002
LOCUS Mus musculus clone RP23-5K17, complete sequence.
DEFINITION AC084382
ACCESSION AC084382.1 GI:15778814
VERSION
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

```

```

REFERENCE
1 (bases 1 to 165077)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 165077)
AUTHORS McPherson,J.D.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-2001) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, Missouri 63108, USA

```

```

REFERENCE
3 (bases 1 to 165077)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA

```

COMMENT

```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M.BA0005K17
-----
Location/Qualifiers
1..165077
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-5K17"

```

FEATURES

```

source
1..165077
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-5K17"

```

ORIGIN

```

Query Match 100.0%; Score 16; DB 10; Length 165077;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GGGCATGCGGGGGG 16
|||||

```

```

Db 29008 GGGCATGCGGGGGG 29023
|||||

```

RESULT 7

```

AC139123 AC139123 183540 bp DNA linear HTG 05-FEB-2003
LOCUS Canis familiaris clone RP81-340C22, WORKING DRAFT SEQUENCE, 10
ordered pieces.
DEFINITION AC139123
ACCESSION AC139123
VERSION AC139123.2 GI:28209437
KEYWORDS HTG; HTGS PHASE2; HTGS_DRAFT.
SOURCE Canis familiaris (dog)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

```

```

REFERENCE
1 (bases 1 to 183540)
AUTHORS Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Carliga,K., Coleman,B., Engle,J., Granite,S., Guan,X., Gupta,J.,
Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E.,
Leric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B.,
Margulies,E.H., Masiello,C., Maskeri,B., McDowell,J.,
Paguirigan,C., Pearson,R., Portnoy,M.E., Prasad,A.,
Raddix-Dugue,N., Schandler,K., Schueler,M.G., Sison,C.,
Stantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Vogt,J.L.,
Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.
TITLE NISC Comparative Sequencing Initiative
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 183540)
AUTHORS Green,E.D.
TITLE Direct Submission
JOURNAL Submitted (24-JAN-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA

```

```

REFERENCE
3 (bases 1 to 183540)
AUTHORS Green,E.D.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA

```

```

COMMENT
On Feb 5, 2003 this sequence version replaced gi:27884878.
----- Genome Center -----
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.zoo@nih.gov
----- Project Information -----
Center project name: eav
Center clone name: 340C22

```

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

```

----- Summary Statistics -----
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 181869 bases at least Q40

```

Consensus quality: 182282 bases at least Q30
 Consensus quality: 182531 bases at least Q20
 Insert size: 174000; agarose-fp
 Insert size: 182640; sum-of-contigs
 Quality coverage: 11.73x in Q20 bases; agarose-fp
 Quality coverage: 11.17x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 1319: contig of 1319 bp in length
 1320 1419: gap of unknown length
 1420 6511: contig of 5092 bp in length
 6512 6611: gap of unknown length
 6612 17980: contig of 11369 bp in length
 17981 18080: gap of unknown length
 18081 61539: contig of 43459 bp in length
 61540 61639: gap of unknown length
 61640 101551: contig of 39912 bp in length
 101552 101651: gap of unknown length
 101652 116778: contig of 15127 bp in length
 116779 116878: gap of unknown length
 116879 156712: contig of 39834 bp in length
 156713 156812: gap of unknown length
 156813 166395: contig of 9483 bp in length
 166396 166395: gap of unknown length
 166396 168306: contig of 2511 bp in length
 168307 168907: gap of unknown length
 168907 183540: contig of 14534 bp in length.

FEATURES

source
 1..183540
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /db_xref="taxon:9615"
 /clone="RP81-340C32"
 /clone_lib="RP81"

misc_feature
 1..138506
 /note="clone overlaps with GenBank Accession Number AC135955 clone RP81-65H2 (center project name cwu)"

misc_feature
 1..1319
 /note="assembly_fragment"
 clone_end:77
 vector_side:left

misc_feature
 1420..6511
 /note="assembly_fragment"

misc_feature
 6612..17980
 /note="assembly_fragment"

misc_feature
 18081..61539
 /note="assembly_fragment"

misc_feature
 61640..101551
 /note="assembly_fragment"

misc_feature
 101652..116778
 /note="assembly_fragment"

misc_feature
 116879..156712
 /note="assembly_fragment"

misc_feature
 156813..166295
 /note="assembly_fragment"

misc_feature
 166396..168906
 /note="assembly_fragment"

misc_feature
 169007..183540
 /note="assembly_fragment"
 clone_end:SP6
 vector_side:right

ORIGIN

Query Match 100.0%; Score 16; DB 2; Length 183540;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGCATGATGGGGG 16
 Db 1020 GGGCATGATGGGGG 1035

RESULT 8

AC131987/c
 AC131987
 LOCUS Mus musculus clone RP24-184L10, WORKING DRAFT SEQUENCE, 8 unordered pieces.
 DEFINITION

ACCESSION

AC131987.3 GI:29294243
 HTG: HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
 KEYWORDS
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Biren,B., Nusbaum,C. and Lander,E.
 Mus musculus, clone RP24-184L10

REFERENCE

1 (bases 1 to 186129)
 Biren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

AUTHORS

Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

Submitted (28-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE

3 (bases 1 to 186129)
 Biren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT

On Mar 27, 2003 this sequence version replaced gi:28273441.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L27107
Center clone name: 184 L 10
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 183983 bases at least Q40
Consensus quality: 184631 bases at least Q30
Consensus quality: 185040 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 185429; sum-of-contigs
Quality coverage: 11.1 in Q20 bases; agarose-fp
Quality coverage: 10.1 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1963: contig of 1963 bp in length
* 1964 2063: gap of 100 bp
* 2064 7095: contig of 5032 bp in length
* 7096 7196: gap of 100 bp
* 7196 20081: contig of 12886 bp in length
* 20082 20181: gap of 100 bp
* 20182 32509: contig of 12328 bp in length
* 32510 32609: gap of 100 bp
* 32610 45123: contig of 12514 bp in length
* 45124 45223: gap of 100 bp
* 45224 73181: contig of 27958 bp in length
* 73182 73281: gap of 100 bp
* 73282 167035: contig of 93754 bp in length
* 167036 167135: gap of 100 bp
* 167136 186129: contig of 18994 bp in length.
----- Location/Qualifiers
source
1. .186129
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone_lib="RP24-184L10"
/clone_lib="RPCI-24 Male Mouse BAC"
1. .1963
/note="assembly_fragment
clone_end:SP6
vector_side:left"
misc_feature
2064..7095
/note="assembly_fragment"
misc_feature
7196..20081
/note="assembly_fragment"
misc_feature
20182..32509
/note="assembly_fragment"
misc_feature
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45224..73181
/note="assembly_fragment"
misc_feature
73282..167035
/note="assembly_fragment"
misc_feature
167136..186129
/note="assembly_fragment
clone_end:T7
vector_side:right"
ORIGIN
Query Match 100.0%; Score 16; DB 2; Length 186129;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCATGTCATGGGGG 16
|||||
DB 173050 GGCATGTCATGGGGG 173035

RESULT 9
CONS1RHC 192462 bp DNA linear PRI 03-MAY-2001
LOCUS Human chromosome 14 DNA sequence BAC R-736N17 of library RPCI-11
DEFINITION from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION AL161669
VERSION AL161669.5 GI:13990665
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 192462)
AUTHORS Heilig, R., Petit, J. L., Vico, V., Dasilva, C., Robert, C., Wincker, P.,
Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,
Levy, M., Eckenberg, R., Bruls, T., Deberardinis, V., Cruaud, C.,
Gyapay, G., Saurin, W. and Weissenbach, J.
TITLE Sequencing of the human chromosome 14
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 192462)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-MAY-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr
On May 8, 2001 this sequence version replaced gi:11611164.
----- Genom Center
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: <http://www.genoscope.cns.fr/>
Contact: Seqref@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-45P15 (AC=AL1138976)
Downstream BAC (overlapping the SP6 end) : C-2538G10
----- Summary Statistics
Assembly program: Phrap, version 2.0
Quality coverage: 10.43x in Q20 bases; sum-of-contigs

Overall quality chart :
Range : bases
0 :
1 - 9 :
10 - 19 : 4
20 - 29 : 9
30 - 39 : 151
40 - 49 : 2414
50 - 59 : 6200
60 - 69 : 8214
70 - 79 : 18797
80 - 89 : 54419
90 - 99 : 102254
Percentage of bases with a quality value >= 40 : 99 %

FEATURES
Location/Qualifiers
1. 192462
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="14"
/clone="R-736N17"
/clone_lib="RPCI-11"
27321..27545
/note="matching EMBL:G04572
STS

AUTHORS

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Dorris, L., Erickson, J., Faro, S., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melidrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

Submitted (27-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 27, 2003 this sequence version replaced gi:28626869.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html

JOURNAL

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

COMMENT

Center project name: L26354
Center clone name: 188 M.21
----- Summary Statistics -----
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 221635 bases at least Q40
Consensus quality: 221908 bases at least Q30
Consensus quality: 221986 bases at least Q20
Insert size: 200000; agarose-fp
Quality coverage: 10.7 in Q20 bases; agarose-fp
Quality coverage: 9.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 2031: contig of 2031 bp in length
* 2032 2131: gap of 100 bp
* 2132 15244: contig of 13113 bp in length
* 15245 15344: gap of 100 bp
* 15345 37649: contig of 22305 bp in length
* 37650 37749: gap of 100 bp
* 37750 148102: contig of 110353 bp in length
* 148103 148202: gap of 100 bp
* 148203 190361: contig of 42159 bp in length
* 190362 190461: gap of 100 bp
* 190462 222510: contig of 32049 bp in length.

FEATURES

Location/Qualifiers
1..222510
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-188M21"
/clone_lib="RPCI-23 Female Mouse BAC"

AUTHORS

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chararo, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzgerald, M., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lebockzy, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Melidrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Viel, R., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 1, 2003 this sequence version replaced gi:28626869.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html

JOURNAL

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

COMMENT

Center project name: L26354
Center clone name: 188 M.21
----- Summary Statistics -----
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 221635 bases at least Q40
Consensus quality: 221908 bases at least Q30
Consensus quality: 221986 bases at least Q20
Insert size: 200000; agarose-fp
Quality coverage: 10.7 in Q20 bases; agarose-fp
Quality coverage: 9.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 2031: contig of 2031 bp in length
* 2032 2131: gap of 100 bp
* 2132 15244: contig of 13113 bp in length
* 15245 15344: gap of 100 bp
* 15345 37649: contig of 22305 bp in length
* 37650 37749: gap of 100 bp
* 37750 148102: contig of 110353 bp in length
* 148103 148202: gap of 100 bp
* 148203 190361: contig of 42159 bp in length
* 190362 190461: gap of 100 bp
* 190462 222510: contig of 32049 bp in length.

FEATURES

Location/Qualifiers
1..222510
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-188M21"
/clone_lib="RPCI-23 Female Mouse BAC"

misc_feature 1. .2031
/note="assembly_fragment"
2132. .15244
misc_feature /note="assembly_fragment"
15345. .37649
misc_feature /note="assembly_fragment"
37750. .148102
misc_feature /note="assembly_fragment"
148203. .190361
misc_feature /note="assembly_fragment"
190462. .222510
misc_feature /note="assembly_fragment
clone_end:T7
vector_side:right"

ORIGIN

Query Match 100.0%; Score 16; DB 2; Length 222510;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16
|||||
Db 32129 GGGCATGCATGGGGG 32144

RESULT 11
AC147160/c
LOCUS AC147160.1 GI:38154247
DEFINITION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
ACCESSION Mus musculus chromosome UNK clone RP24-336A22, WORKING DRAFT
VERSION AC147160
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 227805)
AUTHORS Wilson,R.K.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 227805)
AUTHORS Wilson,R.K.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu
Contact: submission@watson.wustl.edu
----- Project Information -----
Center project name: M_BB0336A22
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: Plasmid; 100%
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 221580 bases at least Q40
Consensus quality: 222826 bases at least Q30
Consensus quality: 223563 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1272: contig of 1272 bp in length
* 1372: gap of unknown length
* 2460: contig of 1088 bp in length
* 2560: gap of unknown length
* 3814: contig of 1254 bp in length
* 3915: gap of unknown length
* 7235: contig of 3321 bp in length
* 7336: gap of unknown length
* 11348: contig of 4013 bp in length
* 11449: gap of unknown length
* 20255: contig of 8806 bp in length
* 20355: gap of unknown length
* 26123: contig of 5768 bp in length
* 26223: gap of unknown length
* 39124: contig of 12901 bp in length
* 39224: gap of unknown length
* 56052: contig of 16828 bp in length
* 56152: gap of unknown length
* 74805: contig of 18653 bp in length
* 74905: gap of unknown length
* 74905: contig of 21795 bp in length
* 96700: gap of unknown length
* 96800: contig of 24548 bp in length
* 121348: gap of unknown length
* 121448: contig of 28522 bp in length
* 149970: gap of unknown length
* 150070: contig of 33002 bp in length
* 183072: gap of unknown length
* 183172: contig of 44634 bp in length.

FEATURES
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP24-336A22"

misc_feature 1. .1272
/note="assembly_name:Contig41"
1373. .2460
misc_feature /note="assembly_name:Contig43"
2561. .3814
misc_feature /note="assembly_name:Contig45"
3915. .7235
misc_feature /note="assembly_name:Contig47"
7336. .11348
misc_feature /note="assembly_name:Contig48"
11449. .20254
misc_feature /note="assembly_name:Contig49"
20355. .26122
misc_feature /note="assembly_name:Contig50"
26223. .39123
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39224. .56051
misc_feature /note="assembly_name:Contig52"
56152. .74804
misc_feature /note="assembly_name:Contig53"
74905. .96699
misc_feature /note="assembly_name:Contig54"
96800. .121347
misc_feature /note="assembly_name:Contig55"
121448. .149969
misc_feature /note="assembly_name:Contig56"
150070. .183071
misc_feature /note="assembly_name:Contig57"
183172. .227805
misc_feature /note="assembly_name:Contig58"

ORIGIN

Query Match 100.0%; Score 16; DB 2; Length 227805;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16

Db 50847 GGGCATGCATGGGGG 50832

|||||

RESULT 12
AC095635
LOCUS
DEFINITION
AC095635 234548 bp DNA linear HTG 09-MAY-2003
Rattus norvegicus clone CH230-8K1, WORKING DRAFT SEQUENCE, 2
unordered pieces.
AC095635 6 GI:30467118
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus
1 (bases 1 to 234548)
Muzry, D., Marie, Metzger, M., Lee, Abranzone, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Ayodeji, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Bernham, P.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, B.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, R., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleaveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, C., Denison, S., Deramo, C., Ding, Y., Din, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escoto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisa, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Georgiev, B., Geer, K., Gill, R., Grady, M., Guerra, T., Guera, M.,
Gunnarsson, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M.,
Hollins, B., Howells, S., Hui, J., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowals, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorenshewa, L., Louisege, H., Izado, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E.,
Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwackelme, O., Okwono, G., Olariupunsegon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,
Plopper, P., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.D.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villanasa, D., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wlecyk, R., Woodson, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
Direct Submission
Unpublished
2 (bases 1 to 234548)
Worley, K.C.
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department

REFERENCE
AUTHORS
TITLE
JOURNAL

of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 234548)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 9, 2003 this sequence version replaced gi:24817791.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GCWM
Center clone name: CH230-8K1
----- Summary Statistics
Assembly program: Atlas
Consensus quality: 22438 bases at least Q40
Consensus quality: 224642 bases at least Q30
Consensus quality: 225972 bases at least Q20
Estimated insert size: 232080; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved
* 1 232993: contig of 232993 bp in length
* 232994 233093: gap of unknown length
* 233094 234548: contig of 1455 bp in length.

FEATURES
source
1. 234548
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-8K1"
1. 1711
/note="wgs_contig"

misc_feature
1 1711
/note="wgs_contig"

ORIGIN
Query Match 100.0%; Score 16; DB 2; Length 234548;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GGGCATGCATGGGGG 16
|||||
Db 114301 GGGCATGCATGGGGG 114316

RESULT 13
AC131337
LOCUS
DEFINITION
AC131337 345420 bp DNA linear HTG 23-APR-2003
Mus musculus clone RP23-480E1, WORKING DRAFT SEQUENCE, 17 unordered

* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

pieces.
AC131337
AC131337.4 GI:30017797
HTG; HTGS; PHASE1; HTGS; DRAFT.
Mus musculus (house mouse)
Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 345420)
Birren,B., Nusbaum,C. and Lander,B.
Mus musculus, clone RP23-480E1
Unpublished
2 (bases 1 to 345420)
Birren,B., Nusbaum,C., Lander,B., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhalter,B.,
Camarata,J., Chang,J., Chararo,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArillano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrum,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.

1221: contig of 1221 bp in length
1222: gap of 100 bp
1322: contig of 1419 bp in length
2840: gap of 100 bp
2841: contig of 1511 bp in length
4351: gap of 100 bp
4352: contig of 2780 bp in length
7231: gap of 100 bp
7232: gap of 100 bp
7332: contig of 6249 bp in length
13580: gap of 100 bp
13680: contig of 554 bp in length
19224: gap of 100 bp
19324: contig of 4921 bp in length
24245: gap of 100 bp
24246: contig of 9959 bp in length
3304: gap of 100 bp
3305: contig of 10555 bp in length
43959: gap of 100 bp
44059: contig of 20133 bp in length
64192: gap of 100 bp
64193: contig of 75941 bp in length
140234: gap of 100 bp
140235: contig of 26604 bp in length
166937: gap of 100 bp
166938: contig of 35527 bp in length
202564: gap of 100 bp
202565: contig of 33201 bp in length
235865: gap of 100 bp
235866: contig of 46274 bp in length
282239: gap of 100 bp
282240: contig of 42901 bp in length
325241: gap of 100 bp
325341: contig of 20080 bp in length.

Location/Qualifiers
1. 345420
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-480E1"
/clone_lib="RPCI-23 Female Mouse BAC"

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1. 1221
/note="assembly_fragment"
1322. 2740
/note="assembly_fragment"
2841. 4351
/note="assembly_fragment"
4452. 7231
/note="assembly_fragment"
7332. 13580
/note="assembly_fragment"
13681. 19224
/note="assembly_fragment"
19325. 24245
/note="assembly_fragment"
24346. 33304
/note="assembly_fragment"
33405. 43959
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44060. 64192
/note="assembly_fragment"
64293. 140233
/note="assembly_fragment"
140334. 166937
/note="assembly_fragment"
167038. 202564
/note="assembly_fragment"
202865. 235865

FEATURES
source

Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 345420)
Birren,B., Nusbaum,C., Lander,B., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavskiy,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cook,A., Cooke,P., Corum,B., DeArillano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafiz,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrum,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (23-APR-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 17, 2003 this sequence version replaced gi:28626850.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submission@genome.wi.mit.edu
----- Project Information
Center project name: L26504
Center clone name: 480_E_1

* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces

```

misc_feature      /note="assembly_fragment"
235966..282239
/note="assembly_fragment"
282340..325240
/note="assembly_fragment"
325341..345420
/note="assembly_fragment"
clone_end:T7
vector_side:right"

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ORIGIN

```

Query Match      100.0%; Score 16; DB 2; Length 345420;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GGGCATGCGATGGGGG 16
|||||

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Db      160990 GGGCATGCGATGGGGG 161005
|||||

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RESULT 14

```

AX251652/c      657 bp      DNA      linear      PAT 05-OCT-2001
LOCUS
DEFINITION      Sequence 47 from Patent WO0168849.
ACCESSION      AX251652
VERSION        AX251652.1 GI:15985065
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE

```

AUTHORS      Wood, L.S., Vogeli, G., Karnovsky, A.M., Ruble, C.L., Linske-O, L.I.,
Wang, J. and Liu, D.
HUMAN Ion channels
Patent: WO 0168849-A 47 20-SEP-2001;
Pharmacia & Upjohn Company (US)

```

FEATURES

```

Source
1..657
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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ORIGIN

```

Query Match      93.8%; Score 15; DB 6; Length 657;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
Qy      1 GGGCATGCGATGGGGG 15
|||||

```

```
Db      550 GGGCATGCGATGGGGG 536
|||||

```

RESULT 15

```

BV013263/c      867 bp      DNA      linear      STS 30-MAY-2003
LOCUS
DEFINITION      S212P6739F510.T0 CZECHII/Ei Mus musculus STS genomic, sequence
tagged site.
ACCESSION      BV013263
VERSION        BV013263.1 GI:31097158
KEYWORDS
SOURCE
Mus musculus (house mouse)

```

ORGANISM

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 867)
Lander, E.S., Lindblad-Toh, K., and Daly, M.J.
Wade, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C.,

```

REFERENCE

```

AUTHORS      Lander, E.S., Lindblad-Toh, K., and Daly, M.J.
The mosaic structure of variation in the laboratory mouse genome
Nature 420 (6915), 574-578 (2002)
22354684
MEDLINE
PUBMED
12466852
COMMENT

```

Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome
Research
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6175521477
Fax: 6175580903
Email: kersli@genome.wi.mit.edu
Primer A: None
Primer B: None
STS size: 867

Protocol:
WGS-discovery: Paired-end low-coverage whole genome shotgun reads
were generated from 125S1/SvImJ, C3H/HeJ, and BALB/cByJ. The WGS
reads were placed uniquely on the MGS CVs C57BL/6J assembly and SNP
detection was carried out by SSAHA-SNP. 225,000 reads were
annotated

as STGs and 81,000 SNPs were annotated with alleles from C57BL/6J
and the strain from which the particular read came. The validation
rate for these SNPs was estimated at approximately 98%.

FEATURES

```

Location/Qualifiers
1..867
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CZECHII/Ei"
/db_xref="taxon:10090"
/map="- 1 28-802 47402426-47401650"
/clone_lib="CZECHII/Ei"
<1..867

```

STS

ORIGIN

```

Query Match      93.8%; Score 15; DB 11; Length 867;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
Qy      1 GGGCATGCGATGGGGG 15
|||||

```

```
Db      99 GGGCATGCGATGGGGG 85
|||||

```

Search completed: July 2, 2004, 10:08:03
Job time : 568.317 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 06:05:50 ; Search time 119.902 Seconds
(without alignments)
566.887 Million cell updates/sec

Title: US-10-068-160-15

Perfect score: 16

Sequence: 1 gggcatgcatgggggg 16

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002s:*
- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15	93.8	657	4	Aad17168 Human ion
C 2	15	93.8	657	7	Ac001553 CDNA clon
C 3	15	93.8	657	9	Ad29244 Novel hum
C 4	15	93.8	2000	7	Ada72822 Rice gene
C 5	14.4	90.0	51	4	Aal31444 Human SNP
C 6	14.4	90.0	390	6	Ab178599 Human ova
C 7	14.4	90.0	408	2	AaQ22507 Human ova
C 8	14.4	90.0	408	2	AaQ22508 K64, P83,
C 9	14.4	90.0	408	2	AaQ22510 Insert fr
C 10	14.4	90.0	408	2	AaQ22506 Lys64, Pr
C 11	14.4	90.0	462	8	Ach19351 Human adu
C 12	14.4	90.0	475	8	Ach33855 Human end
C 13	14.4	90.0	675	2	Aav33946 Gibbon in
C 14	14.4	90.0	865	1	Aan80502 Sequence
C 15	14.4	90.0	909	1	Aan92339 Single st
C 16	14.4	90.0	1653	6	Ab54810 Human ova
C 17	14.4	90.0	1662	2	Aat84711 Human Snc
C 18	14.4	90.0	2001	6	Aas94988 Human DNA
C 19	14.4	90.0	2109	7	AcD19383 CDNA enco
C 20	14.4	90.0	2529	6	Ab169709 Prostate
C 21	14.4	90.0	2529	6	Ab10905 Human bre
C 22	14.4	90.0	2529	8	AdB70327 Keratin 5
C 23	14.4	90.0	2529	9	AdB75393 Prostate

ALIGNMENTS

RESULT 1

AAD17168/c

ID AAD17168 standard; CDNA; 557 BP.

XX AAD17168;

AC AAD17168;

XX 29-NOV-2001 (first entry)

XX Human ion channel-91 (ion91) CDNA.

XX Human; ion channel-91; ion91; antiinflammatory; immunosuppressive;
analgesic; nootropic; neuroprotective; antidepresant; cardiant;
cytostatic; antiviral; human immunodeficiency virus; HIV; anorectic;
antiviral; thyroid disorder; thyrotoxicosis; myxoedema; renal failure;
Crohn's disease; rheumatoid arthritis; autoimmune disorder; pain; stroke;
Psychotic disorder; neurological disorder; anxiety; dyskinesia;
KW Huntington's disease; degenerative disorder; Parkinson's disease;
KW schizophrenia; Alzheimer's disease; cardiovascular disease; cancer;
KW metabolic disorder; anorexia; obesity; mental disorder; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 141..455

FT /*tag= a

FT /product= "Human ion91 protein"

FT /transl_except= {pos:333..341, aa:Ser-Pro}

FT /note= "This translational exception comprises an in-

frame stop codon insertion; CDS does not include start

and stop codon"

FT /partial

XX WO200168849-A2.

XX 20-SEP-2001.

XX 09-MAR-2001; 2001WO-US007503.

XX 10-MAR-2000; 2000US-0188400P.

XX 10-MAR-2000; 2000US-0188517P.

XX 10-MAR-2000; 2000US-0188518P.

XX 10-MAR-2000; 2000US-0188519P.

XX 05-JUL-2000; 2000US-0215815P.

XX 06-JUL-2000; 2000US-0216481P.

XX (PAAA) PHARMACIA & UPJOHN CO.

XX Wood LS, Vogeli G, Karnovsky AM, Ruble CL, Linske-O'Connell LI;
 PI Wang J, Liu D;
 XX WPI; 2001-565795/63.
 DR P-PSDB; AAE10116.
 XX
 XX New ion channel polynucleotides and polypeptides, useful for
 PT identification of ion channel modulators and treatment of mental
 PT disorders, infections, cancer and autoimmune diseases.
 XX
 XX Claim 3; Page 99; 188pp; English.
 XX
 CC The patent discloses novel human ion channel polypeptides and their
 CC corresponding polynucleotides. The ion channel sequences and their
 CC modulators are used for the treatment of viral infections (e.g. human
 CC immunodeficiency virus (HIV)), thyroid disorders (e.g., Crohn's
 CC myxoedema), renal failure, inflammatory conditions (e.g., Crohn's
 CC disease), rheumatoid arthritis, autoimmune disorders, pain, stroke,
 CC psychotic and neurological disorders (e.g. anxiety, depression and
 CC schizophrenia), dyskinesias (e.g. Huntington's disease), degenerative
 CC disorders (e.g., Parkinson's disease, Alzheimer's disease), cardio-
 CC vascular diseases, cancer, metabolic disorders (e.g. anorexia, obesity)
 CC and mental disorders. The present sequence is a cDNA encoding human ion
 CC channel-91 (ion91) protein
 XX
 XX Sequence 657 BP; 134 A; 217 C; 175 G; 131 T; 0 U; 0 Other;
 SQ
 Query Match 93.8%; Score 15; DB 4; Length 657;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGCATGCATGGGG 15
 Db 550 GGGCATGCATGGGG 536
 RESULT 2
 AC001553/c
 ID AC001553 standard; cDNA; 657 BP.
 XX AC001553;
 XX
 DT 29-JUL-2003 (first entry)
 XX
 DE cDNA clone Ion91 encoding human ion channel.
 XX
 KW Human; ion channel; immune response; RFLP; genetic mapping;
 KW restriction fragment length polymorphism; viral infection;
 KW inflammatory condition; Crohn's disease; homeostasis; cancer;
 KW rheumatoid arthritis; autoimmune disorder; CNS disorder; dementia;
 KW central nervous system disorder; Huntington's disease; virucide;
 KW degenerative disorder; Parkinson's disease; Alzheimer's disease;
 KW cardiovascular disease; myocardial infarction; hormonal disorder;
 KW transcription factor; antiinflammatory; antirheumatic; antiarthritic;
 KW immunosuppressive; neurotropic; anticonvulsant; antiparkinsonian;
 KW neuroprotective; cardiant; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003023014-A2.
 XX
 PD 20-MAR-2003.
 XX
 XX 12-SEP-2002; 2002WO-US029087.
 XX
 PR 12-SEP-2001; 2001US-0318733P.
 PR 13-AUG-2002; 2002US-0403254P.
 XX
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX
 XX Robertds SL, Benjamin CW, Karnovsky AM, Ruble CL;
 PI
 XX

DR WPI: 2003-313250/30.
 DR P-PSDB; ABO97377.
 XX
 PT Novel human ion channel polypeptide, useful for inducing an immune
 PT response in a mammal and for treating disease or conditions related to
 PT central nervous system and cancer.
 PT
 PS
 XX Example 1; Page 103; 146pp; English.
 XX
 CC The present invention relates to the isolation of novel human ion channel
 CC polypeptides, and the polynucleotide sequences encoding them. The human
 CC ion channel polypeptides are useful for inducing an immune response in a
 CC mammal, and for identifying a compound which binds to and/or modulates
 CC the ion channel. The polynucleotide sequences encoding human ion channel
 CC polypeptides are useful for screening restriction fragment length
 CC polymorphisms (RFLPs) associated with certain disorders, and for genetic
 CC mapping. The human ion channel polypeptide and polynucleotide sequences
 CC are useful in the treatment of diseases or conditions such as viral
 CC infections, inflammatory conditions (e.g. Crohn's disease), diseases
 CC related to homeostasis, rheumatoid arthritis, autoimmune disorders,
 CC central nervous system (CNS) disorders (e.g. dementia, Huntington's
 CC disease), degenerative disorders (e.g. Parkinson's and Alzheimer's
 CC disease), cardiovascular diseases (e.g. myocardial infarction), cancer,
 CC and hormonal disorders. The polynucleotide sequences are useful to design
 CC novel transcription factors for modulating the expression of human ion
 CC polypeptides in native cells, and cells transformed or transfected with
 CC them. The present sequence represents a cDNA clone encoding a human ion
 CC channel polypeptide
 XX
 XX Sequence 657 BP; 134 A; 217 C; 175 G; 131 T; 0 U; 0 Other;
 SQ
 Query Match 93.8%; Score 15; DB 7; Length 657;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGCATGCATGGGG 15
 Db 550 GGGCATGCATGGGG 536
 RESULT 3
 ADE29244/c
 ID ADE29244 standard; cDNA; 657 BP.
 XX ADE29244;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Novel human ion channel ion-91 cDNA.
 XX
 KW neurotropic; neuroprotective; neuroleptic; immunosuppressive; cardiant;
 KW antiarteriosclerotic; antiinflammatory; antidepressant; antiarthritic;
 KW ophthalmological; cycostatic; hypertensive; hypotensive; vasotropic;
 KW antimigraine; analgesic; antiparkinsonian; thrombolytic; antithyroid;
 KW ion channel; ion-x; brain disorder; mental disorder; schizophrenia;
 KW depression; anxiety; attention deficit hyperactivity disorder; migraine;
 KW stroke; neurodegenerative disease; Alzheimer's disease;
 KW Parkinson's disease; glaucoma; macular degeneration;
 KW cardiovascular disease; ischaemia; congestive heart failure; arrhythmia;
 KW high blood pressure; restenosis; thyroid disorder; renal failure;
 KW inflammatory condition; autoimmune disorder; rheumatoid arthritis;
 KW movement disorder; central nervous system disorder; infection;
 KW eating disorder; cardiovascular disorder; thrombosis; atherosclerosis;
 KW proliferative disorder; cancer; hormonal disorder; sexual dysfunction;
 KW Gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003190714-A1.
 XX
 PD 09-OCT-2003.
 XX
 XX 09-MAR-2001; 2001US-00302668.
 PF

XX 10-MAR-2000; 2000US-0188400P.
PR 10-MAR-2000; 2000US-0188484P.
PR 10-MAR-2000; 2000US-0188517P.
PR 10-MAR-2000; 2000US-0188518P.
PR 10-MAR-2000; 2000US-0188519P.
PR 05-JUL-2000; 2000US-0215815P.
PR 06-JUL-2000; 2000US-0216481P.
XX (ROBE/) ROBERTS S L.
PA (BENJ/) BENJAMIN C W.
PA (KARN/) KARNOVSKY A M.
PA (RUBL/) RUBLE C L.
PA (LINS/) LINSKE-O'CONNELL L I.
PA (WANG/) WANG.
PA (LIUD/) LIU D.
XX
PI Robert SL, Benjamin CW, Karnovsky AM, Ruble CL;
PI Linske-O'connell LI, Wang J, Liu D;
XX
DR WPI; 2003-875311/81.
DR P-PSDB; ADB29295.
XX
XX New nucleic acid sequences encoding ion channels are useful to detect and
PT treat human diseases and conditions, particularly of the brain,
PT especially mental disorders.
XX
PS Claim 4; SEQ ID NO 47; 105pp; English.
XX
CC The invention describes an isolated nucleic acid comprising a sequence
CC encoding at least a portion of an ion channel (ion-x). The invention is
CC useful to detect and treat diseases and conditions of the brain,
CC particularly mental disorders, including schizophrenia, depression,
CC anxiety, attention deficit hyperactivity disorder, migraine, stroke, and
CC neurodegenerative diseases such as Alzheimer's disease, Parkinson's
CC disease, glaucoma and macular degeneration, cardiovascular diseases such
CC as ischaemia, congestive heart failure, arrhythmia, high blood pressure
CC and restenosis. The invention may also be used to detect or treat thyroid
CC disorders, renal failure, inflammatory conditions, autoimmune disorders
CC including rheumatoid arthritis, movement disorders, central nervous
CC system disorders, infections, eating disorders, cardiovascular disorders
CC including thrombosis and atherosclerosis, and proliferative disorders such
CC as cancers, hormonal disorders and sexual dysfunction. This sequence
CC encodes a novel ion channel.
XX
SQ Sequence 657 BP; 134 A; 217 C; 175 G; 131 T; 0 U; 0 Other;
Query Match 93.8%; Score 15; DB 9; Length 657;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCATGCGATGGGG 15
DB 550 GGGCATGCGATGGGG 536
RESULT 4
ADA72822/c
ID ADA72822 standard; DNA; 2000 BP.
XX
AC ADA72822;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 6147.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX
OS Oryza sativa.
XX
PN WO2003000898-A1.
XX

PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 27; SEQ ID NO 6147; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 2000 BP; 527 A; 468 C; 501 G; 503 T; 0 U; 1 Other;
Query Match 93.8%; Score 15; DB 7; Length 2000;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCATGCGATGGGG 15
DB 1856 GGGCATGCGATGGGG 1842
RESULT 5
AAL31444
ID AAL31444 standard; DNA; 51 BP.
XX
AC AAL31444;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #4652.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
PA

XX Shimkets RA, Leach M;
 XX WPI; 2001-465210/50.
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
 PT autoimmune diseases and infections.
 XX Claim 1; Page 2724; 4143pp; English.
 XX The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
 CC protein coupled receptors and cholesteraes. The present sequence is one
 CC such oligonucleotide. The oligonucleotides and the peptides encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of the proteins listed above.
 CC Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms
 XX SQ Sequence 51 BP; 13 A; 7 C; 29 G; 2 T; 0 U; 0 Other;
 Query Match 90.0%; Score 14.4; DB 4; Length 51;
 Best Local Similarity 93.8%; Pred. No. 7.8e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGGCATGCGATGGGGG 16
 DB 34 GGGCAGGCGATGGGGG 49
 RESULT 6
 ID ABL78599 standard; cDNA; 390 BP.
 XX ABL78599;
 XX 17-MAY-2002 (first entry)
 XX Human ovarian cancer related cDNA clone SEQ ID NO:1577.
 XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
 XX Homo sapiens.
 XX WO200192581-A2.
 XX 06-DEC-2001.
 XX 29-MAY-2001; 2001WO-US017756.
 XX 26-MAY-2000; 2000US-0207484P.
 XX (CORI-) CORIXA CORP.
 XX Algate PA, Harlocker SL, Jones R;
 XX WPI; 2002-122075/16.
 XX Composition for therapy and diagnosis of ovarian cancer comprising
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
 PT polypeptide, antibody specific to polypeptide or T cell expressing
 PT polypeptide.
 XX Claim 1; SEQ ID NO 1577; 489pp; English.

XX The present invention describes a composition (I) comprising: carriers
 CC and immunostimulants; and a polypeptide (II) of a ovarian tumour
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1)
 CC from the 10912 nucleotide sequences as given in ABL77023 to ABL87934,
 CC (III) encoding (II) having a sequence (S2), a T cell population of (II),
 CC or antigen presenting cells that express (II). (I) has cytostatic
 CC activity. An oligonucleotide (IV) that hybridises to (S1) can be used for
 CC detecting ovarian cancer in a patient's biological sample preferably
 CC serum or ovarian tissue. The method comprises contacting a biological
 CC sample from a patient with (IV), detecting the amount of polynucleotide
 CC hybridising to (IV) and comparing the amount to a predetermined cutoff
 CC value and thereby detecting ovarian cancer in the patient, where the
 CC amount of polynucleotide hybridising to (IV) is detected preferably by
 CC polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is
 CC useful for stimulating and/or expanding T cells specific for an ovarian
 CC tumour protein comprising contacting T cells with (III) or (II). (III) is
 CC useful in design and preparation of ribozyme molecules for inhibiting
 CC expression of the tumour polypeptides and proteins in tumour cells; and
 CC to isolate a full length gene from a suitable library e.g., a tumour cDNA
 CC library using well known techniques
 XX SQ Sequence 390 BP; 83 A; 144 C; 95 G; 64 T; 0 U; 4 Other;
 Query Match 90.0%; Score 14.4; DB 6; Length 390;
 Best Local Similarity 93.8%; Pred. No. 8.8e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGGCATGCGATGGGGG 16
 DB 229 GGGCATGCGATGGGGG 244
 RESULT 7
 ID AAQ22507/C
 XX AAQ22507 standard; DNA; 408 BP.
 XX AC AAQ22507;
 XX 04-SEP-1992 (first entry)
 XX Lys64, Pro83, Met88 Arg99 hIL-35 coding sequence.
 XX Human; interleukin-3; bone marrow transplant; graft; platelet;
 XX hIL-35 derivative.
 XX Homo sapiens.
 XX JP04063595-A.
 XX 28-FEB-1992.
 XX 19-OCT-1990; 90JP-00279108.
 XX 03-APR-1990; 90JP-00087468.
 XX (KIRI) KIRIN BREWERY KK.
 XX WPI; 1992-120155/15.
 XX P-PSDB; AAR22819.
 XX Human interleukin 3 deriv. and its prepn. - for supplementing bone marrow
 PT transplantation and increasing platelet count.
 XX Disclosure; Fig 7; 21pp; Japanese.
 XX This sequence codes for a derivative of human IL-3 having amino acids
 CC Arg, Leu and His at positions 64, 83, 88 and 99, respectively,
 CC substituted by Lys, Pro, Met and Arg. The derivative has a higher
 CC activity than native IL-3. See AAR22813-4, AAQ22503-Q22510 and AAQ22513
 XX Sequence 408 BP; 129 A; 105 C; 87 G; 87 T; 0 U; 0 Other;

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Query Match          90.0%; Score 14.4; DB 2; Length 408;
Best Local Similarity 93.8%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16
DB 261 GGGCAGGCATGGGGG 246

RESULT 8
AAQ22508/c
ID AAQ22508 standard; DNA; 408 BP.
XX AC AAQ22508;
XX DT 04-SEP-1992 (first entry)
XX DE X64, P83, M88, K113, E122, M127, R132, S134 hIL-3 coding sequence.
XX KW Human; interleukin-3; bone marrow transplant; graft; platelet;
XX KW hIL-36 derivative; ss.
XX OS Homo sapiens.
XX PN JP04063595-A.
XX PD 28-FEB-1992.
XX PF 19-OCT-1990; 90JP-00279108.
XX PR 03-APR-1990; 90JP-00087468.
XX PA (KIRI } KIRIN BREWERY KK.
XX DR WPI; 1992-120155/15.
XX PT Human interleukin 3 deriv. and its prepn. - for supplementing bone marrow
XX PT transplantation and increasing platelet count.
XX PS Disclosure; Fig 8; 21pp; Japanese.
XX CC This sequence codes for a derivative of human IL-3 in which Arg, Leu,
XX CC Leu, Thr, Ala, Thr, Ala and Phe at positions 64, 83, 88, 113, 122, 127,
XX CC 132 and 134 have been substituted. The derivative has a higher activity
XX CC than native IL-3. See AAR22813-4, AAQ22503-Q22510 and AAQ22513
XX SQ Sequence 408 BP; 133 A; 102 C; 86 G; 87 T; 0 U; 0 Other;

Query Match          90.0%; Score 14.4; DB 2; Length 408;
Best Local Similarity 93.8%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16
DB 261 GGGCAGGCATGGGGG 246

RESULT 9
AAQ22510/c
ID AAQ22510 standard; DNA; 408 BP.
XX AC AAQ22510;
XX DT 04-SEP-1992 (first entry)
XX DE Insert from plasmid pCGS8 used to construct hIL-3 derivs.
XX KW Human; interleukin-3; bone marrow transplant; graft; platelet;
XX KW sticky end; ds.
XX OS Homo sapiens.

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PN JP04063595-A.
XX 28-FEB-1992.
XX 19-OCT-1990; 90JP-00279108.
XX 03-APR-1990; 90JP-00087468.
XX (KIRI } KIRIN BREWERY KK.
XX WPI; 1992-120155/15.
XX Human interleukin 3 deriv. and its prepn. - for supplementing bone marrow
XX transplantation and increasing platelet count.
XX Example 1; Fig 19; 21pp; Japanese.
XX The 5' end of this strand overhangs the 3' end of the complementary strand
XX by 4 bases; the 5' end of the complementary strand overhangs this strand
XX by the tetranucleotide sequence 5'-AATT-3'. The insert is used in the
XX construction of plasmid pCGS8, which is in turn used in the construction
XX of plasmids coding for human IL-3 derivs. See AAR22813-4, AAQ22503-Q22510
XX and AAQ22513
XX SQ Sequence 408 BP; 126 A; 104 C; 90 G; 88 T; 0 U; 0 Other;

Query Match          90.0%; Score 14.4; DB 2; Length 408;
Best Local Similarity 93.8%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16
DB 248 GGGCAGGCATGGGGG 233

RESULT 10
AAQ22506/c
ID AAQ22506 standard; DNA; 408 BP.
XX AC AAQ22506;
XX DT 04-SEP-1992 (first entry)
XX DE Lys64, Pro83, Met88 hIL-3 coding sequence.
XX KW Human; interleukin-3; bone marrow transplant; graft; platelet;
XX KW hIL-34 derivative.
XX OS Homo sapiens.
XX PN JP04063595-A.
XX 28-FEB-1992.
XX 19-OCT-1990; 90JP-00279108.
XX 03-APR-1990; 90JP-00087468.
XX (KIRI } KIRIN BREWERY KK.
XX WPI; 1992-120155/15.
XX P-PSDB; AAR22818.
XX Human interleukin 3 deriv. and its prepn. - for supplementing bone marrow
XX transplantation and increasing platelet count.
XX Disclosure; Fig 6; 21pp; Japanese.
XX This sequence codes for a derivative of human IL-3 having amino acids
XX Arg, Leu and Ile at positions 64, 83 and 88, respectively, substituted by
XX Lys, Pro and Met. The derivative has a higher activity than native IL-3.
XX See AAR22813-4, AAQ22503-Q22510 and AAQ22513

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SQ Sequence 408 BP; 130 A; 105 C; 86 G; 87 T; 0 U; 0 Other;
 Query Match 90.0%; Score 14.4; DB 2; Length 408;
 Best Local Similarity 93.8%; Pred. No. 8.8e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16
 DB 261 GGGCAGCATGGGGG 246

RESULT 11
 ACH19351/c
 ID ACH19351 standard; cDNA; 462 BP.
 XX AC ACH19351;
 XX DT 13-OCT-2003 (first entry)
 XX DE Human adult lung cDNA #354.
 XX KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
 KW Genome mapping; biodiversity; genetic disorder.
 XX OS Homo sapiens.
 XX PN US2003073623-A1.
 XX PD 17-APR-2003.
 XX PF 30-JUL-2001; 2001US-00918995.
 XX PR 30-JUL-2001; 2001US-00918995.
 XX PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 XX PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
 XX WPI; 2003-615964/58.
 XX New polynucleotide sequences obtained from various cDNA libraries, useful
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene
 PT mapping, in the recombinant production of protein, or in generating
 PT antisense DNA or RNA.
 XX Claim 1; SEQ ID NO 6563; 44pp; English.
 XX The invention relates to an isolated polynucleotide comprising any one of
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 CC determined by the technique of SBH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations
 CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide
 CC is useful for generating antibodies specific for it. The present sequence
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20030073623
 XX SQ Sequence 462 BP; 89 A; 157 C; 141 G; 71 T; 0 U; 4 Other;

Query Match 90.0%; Score 14.4; DB 8; Length 462;
 Best Local Similarity 93.8%; Pred. No. 8.8e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16
 DB 275 GGGCATCCATGGGGG 260

RESULT 12
 ACH33855/c
 ID ACH33855 standard; cDNA; 475 BP.
 XX AC ACH33855;
 XX DT 13-OCT-2003 (first entry)
 XX DE Human endothelial cell cDNA #1988.
 XX KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
 KW genome mapping; biodiversity; genetic disorder.
 XX OS Homo sapiens.
 XX PN US2003073623-A1.
 XX PD 17-APR-2003.
 XX PF 30-JUL-2001; 2001US-00918995.
 XX PR 30-JUL-2001; 2001US-00918995.
 XX PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 XX PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
 XX WPI; 2003-615964/58.
 XX New polynucleotide sequences obtained from various cDNA libraries, useful
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene
 PT mapping, in the recombinant production of protein, or in generating
 PT antisense DNA or RNA.
 XX Claim 1; SEQ ID NO 21067; 44pp; English.
 XX The invention relates to an isolated polynucleotide comprising any one of
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 CC determined by the technique of SBH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations
 CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide
 CC is useful for generating antibodies specific for it. The present sequence
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20030073623
 XX SQ Sequence 475 BP; 92 A; 160 C; 119 G; 104 T; 0 U; 0 Other;

Query Match 90.0%; Score 14.4; DB 8; Length 475;
 Best Local Similarity 93.8%; Pred. No. 8.9e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 340 GGGCAGGCATGGGGG 325

RESULT 13

AAV33946/C
ID AAV33946 standard; cDNA; 675 BP.

XX AC AAV33946;
XX 15-FEB-1999 (first entry)

XX DE Gibbon interleukin-3 cDNA.

XX KW Panconi anaemia complementation group C; PAC; apoptosis; haematopoiesis;
XX KW bone marrow; chemotherapy; gene therapy; interleukin-3; gibbon;
XX KW His-ILFAC; ds.

XX OS Hylobates lar.

XX FH Key Location/Qualifiers
XX CDS 1..468
XX FT /*tag= a

XX PN W0851792-A1.

XX PD 19-NOV-1998.

XX PF 15-MAY-1998; 98WO-US009975.

XX PR 15-MAY-1997; 97US-0046546P.

XX PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX PI Youssoufian H;

XX DR WPI; 1999-009774/01.

XX DR P-PSDB; AAW68547.

XX PT New conjugate of Panconi anaemia molecule and peptide selective for
XX PT haematopoietic precursor cells - inhibits apoptosis of these cells, for
XX PT treating Panconi anaemia and patients undergoing high-dose chemotherapy
XX PT for cancer.

XX PS Example 1; Page 48-49; 72pp; English.

XX CC This cDNA clone includes a coding region for gibbon interleukin-3 (IL3,
XX CC see AAW68546). IL3 selectively binds to receptors on the surface of
XX CC haematopoietic progenitor cells (HPC) and is transported into the cells
XX CC by endocytosis. The invention provides conjugates, including fusion
XX CC proteins, comprising human Panconi anaemia complementation group C (PAC)
XX CC protein (see AAW68546) and a targeting molecule such as gibbon IL3.
XX CC These conjugates can be expressed e.g. in E. coli host cells utilising
XX CC vectors encoding His-tagged IL3-PAC (termed His-ILFAC) fusions. The
XX CC conjugate, or a nucleic acid encoding it, can be used to deliver PAC to
XX CC an HPC, specifically to inhibit apoptosis, particularly in patients
XX CC exposed to high doses of chemotherapy for treatment of non-malignant
XX CC cancers, also to treat Panconi anaemia (by complementation of the genetic
XX CC defect). Treatment of HPC is done in vitro, ex vivo (e.g. for recombinant
XX CC production of conjugate in cell cultures) or in vivo. Treatment with PAC
XX CC may eliminate the need for extensive bone marrow transplants to restore
XX CC haematopoiesis after chemotherapy

XX SQ Sequence 675 BP; 187 A; 192 C; 138 G; 158 T; 0 U; 0 Other;

Query Match

Best Local Similarity 90.0%; Score 14.4; DB 2; Length 675;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16

Db 324 GGGCAGGCATGGGGG 309

RESULT 14

AAAN80502/C
ID AAN80502 standard; cDNA; 865 BP.

XX AC AAN80502;

XX 25-MAR-2003 (revised)

XX DT 06-DEC-1990 (first entry)

XX DE Sequence encoding gibbon ape leukemia virus-infected gibbon T-cell line
XX DE UCD-144-MLA colony stimulating factor-80 (CSF-80).

XX KW Haematopoietic growth factor; lymphokine; interleukin-3; therapy;

XX KW diagnosis; ss.

XX OS Gibbon.

XX FH Key Location/Qualifiers
XX CDS 35..91

XX FT /*tag= a

XX FT /product= "Leader secretory sequence"

XX FT mat_peptide 92..493

XX FT /*tag= b

XX PN W08800598-A.

XX PD 28-JAN-1988.

XX PF 13-JUL-1987; 87WO-US001702.

XX PR 14-JUL-1986; 86US-00885060.

XX PR 06-AUG-1986; 86US-00893764.

XX PR 07-OCT-1986; 86US-00916335.

XX PR 04-MAR-1987; 87US-00021865.

XX PA (GEMY) GENETICS INST INC.

XX PI Clark SC, Ciarletta AB, Yang YC;

XX DR WPI; 1988-036434/05.

XX DR P-PSDB; AAP80502.

XX PT Primate IL-3 haematopoietic growth factors - used for treating disease
XX PT states due to immune cell or haematopoietic cell deficiency.

XX PS Disclosure; ges 7-8; 51pp; English.

XX CC Non-coding portions may have a regulatory role in transcription in the
XX CC natural host. The 3'-end contains an AT-rich segment including several
XX CC repeats of the sequence ATTAA, which is believed to be related to the RNA
XX CC message stability. DNA sequence was used as a probe to obtain a 674bp DNA
XX CC sequence from a human genomic library (AAN80503). (Updated on 25-MAR-2003
XX CC to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 865 BP; 235 A; 224 C; 179 G; 227 T; 0 U; 0 Other;

QY 1 GGGCATGCATGGGGG 15

Db 349 GGGCAGGCATGGGGG 334

RESULT 15

AAAN92339/C
ID AAN92339 standard; DNA; 909 BP.

XX AC AAN92339;

XX 25-MAR-2003 (revised)

XX DT 16-MAR-1990 (first entry)

Search completed: July 2, 2004, 08:31:35
Job time : 121.902 secs

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:09:30 ; Search time 25,0732 Seconds
(without alignments)
354.132 Million cell updates/sec

Title: US-10-068-160-15

Perfect score: 16

Sequence: 1 gggcatgcattggggg 16

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

1: /cgm2_6/ptodata/2/ina/5A COMB.seq.*

2: /cgm2_6/ptodata/2/ina/5B COMB.seq.*

3: /cgm2_6/ptodata/2/ina/6A COMB.seq.*

4: /cgm2_6/ptodata/2/ina/6B COMB.seq.*

5: /cgm2_6/ptodata/2/ina/PTUS COMB.seq.*

6: /cgm2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.4	90.0	768	4	US-09-252-991A-1689
C 2	14.4	90.0	1662	3	US-08-807-342B-3
C 3	14.4	90.0	3079	4	US-09-643-597-116
C 4	14.4	90.0	3079	4	US-09-480-884A-116
C 5	14.4	90.0	3079	4	US-09-542-635A-116
C 6	14.4	90.0	3079	4	US-09-606-421B-116
C 7	14.4	90.0	3079	4	US-09-221-107-116
C 8	14.4	90.0	3673	4	US-09-266-225D-5
C 9	14.4	90.0	4866	1	US-08-110-158-5
C 10	13.4	83.8	242	4	US-09-397-787-54
C 11	13.4	83.8	481	4	US-09-621-976-10744
C 12	13.4	83.8	684	4	US-09-252-991A-2852
C 13	13.4	83.8	1536	4	US-09-180-109A-3
C 14	13.4	83.8	1930	4	US-09-724-864-9
C 15	13.4	83.8	2000	4	US-09-055-285A-3
C 16	13.4	83.8	2403	4	US-09-023-655-1226
C 17	13.4	83.8	2403	3	US-08-985-908-25
C 18	13.4	83.8	2517	3	US-08-985-908-30
C 19	13.4	83.8	2539	4	US-09-620-312D-454
C 20	13.4	83.8	4368	1	US-08-026-138E-17
C 21	13.4	83.8	4392	1	US-08-026-138E-5
C 22	13.4	83.8	4446	1	US-08-026-138E-6
C 23	13.4	83.8	4808	2	US-08-231-193A-10
C 24	13.4	83.8	4808	2	US-08-486-273A-10
C 25	13.4	83.8	4808	2	US-08-940-086A-10
C 26	13.4	83.8	4808	4	US-08-940-035A-10
C 27	13.4	83.8	4808	4	US-08-935-105A-10

28	13.4	83.8	4808	4	US-09-648-797-10
29	13.4	83.8	4808	4	US-09-386-123-10
30	13.4	83.8	4858	3	US-08-436-332B-9
31	13.4	83.8	6151	4	US-08-217-704C-1
32	13.4	83.8	111282	4	US-09-754-250-3
33	13.4	83.8	319608	4	US-09-539-333D-1
34	13.4	83.8	319608	4	US-09-679-409-1
35	13	81.2	400	4	US-08-956-171E-2996
36	13	81.2	1899	4	US-09-328-352-659
37	13	81.2	3545	3	US-08-480-474-10
38	12.8	80.0	143	4	US-09-025-769B-263
39	12.8	80.0	276	4	US-09-313-294A-1580
40	12.8	80.0	290	4	US-09-702-705-264
41	12.8	80.0	290	4	US-09-736-457-264
42	12.8	80.0	290	4	US-09-614-124B-264
43	12.8	80.0	290	4	US-09-671-325-264
44	12.8	80.0	290	4	US-09-589-184-264
45	12.8	80.0	378	4	US-09-489-039A-4088

ALIGNMENTS

RESULT 1

US-09-252-991A-1689/c

; Sequence 1689, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 1689

; LENGTH: 768

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-1689

Query Match 90.0%; Score 14.4; DB 4; Length 768;

Best Local Similarity 93.8%; Pred. No. 1.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGCATGCATGGGGGG 16

Db 352 GGGCATGCATGGGGGG 337

RESULT 2

US-08-807-342B-3

; Sequence 3, Application US/08807342B

; Patent No. 6077686

; GENERAL INFORMATION:

; APPLICANT: Der, Channing

; APPLICANT: O'Bryan, John P.

; APPLICANT: Pawson, Anthony

; TITLE OF INVENTION: No. 6077686el SHC Proteins

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Howson and Howson

; STREET: Spring House Corporate Cntr., P.O. Box 457

; CITY: Spring House

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19477

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:38:45 ; Search time 1198.24 Seconds
(without alignments)
398.746 Million cell updates/sec

Title: US-10-068-160-15
Perfect score: 16
Sequence: 1 999catgcatg999999 16

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: em_estb.*
2: em_esthm.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_man.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vri.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	16	100.0	178	29	CE070440 tigr-gss-
2	16	100.0	312	9	AA808746 oe56h05.s
3	16	100.0	373	14	CB010201 LB18G01 m
4	16	100.0	399	14	CB010108 LB16E11 m

C 5	16	100.0	422	9	AA798510
C 6	16	100.0	423	9	AA798509
C 7	16	100.0	507	28	BZ317770
C 8	16	100.0	525	28	BZ308462
C 9	16	100.0	526	29	CNS07EQ7
C 10	16	100.0	531	29	CE663190 tigr-gss-
C 11	16	100.0	551	28	BZ323566 ia79g11.g
C 12	16	100.0	577	28	BH877725 hr54e02.g
C 13	16	100.0	645	28	BZ308895 id76f05.d
C 14	16	100.0	667	28	BZ371261 ie33b08.b
C 15	16	100.0	673	28	BZ413880 if18e05.g
C 16	16	100.0	674	28	BH881300 hv24f11.b
C 17	16	100.0	683	9	AW044282 wv67a11.x
C 18	16	100.0	690	28	BZ966328 PUGS75TD
C 19	16	100.0	690	28	BZ994883 PUGK75TB
C 20	16	100.0	696	28	BZ374394 ie24d06.g
C 21	16	100.0	720	28	BZ416253 if65c08.g
C 22	16	100.0	721	28	BZ416263 if65d07.g
C 23	16	100.0	769	28	CC400096 PUHRF48TB
C 24	16	100.0	796	28	BZ416255 if65c10.g
C 25	16	100.0	797	28	BZ416245 if65b11.g
C 26	16	100.0	835	13	BX347138
C 27	16	100.0	836	28	BZ792665 PUGS95TD
C 28	16	100.0	847	29	CG129135 PUFQ559TB
C 29	16	100.0	859	14	CD384067 PTMM09239
C 30	16	100.0	925	13	BX348859 BX348859
C 31	16	100.0	933	13	BX371748 BX371748
C 32	16	100.0	938	28	BZ792664 PUGS95TB
C 33	16	100.0	1065	13	BX338228 BX338228
C 34	16	100.0	1125	13	BUS11621 AGENCOURT
C 35	16	100.0	1201	9	AL523531 AL523531
C 36	16	100.0	1201	13	BX356439 BX356439
C 37	15.2	95.0	538	29	CMS04HG3 Tetraodon
C 38	15	93.8	217	12	BI898692 480406 MA
C 39	15	93.8	273	14	W23910 zb47a07.r1
C 40	15	93.8	288	14	F22293 HSPD07000 H
C 41	15	93.8	341	14	F20981 HSPD05425 H
C 42	15	93.8	379	12	BI133004 daif9f08
C 43	15	93.8	395	9	AA406068 zu67b04.s
C 44	15	93.8	424	9	AA496072 zu67b04.r
C 45	15	93.8	449	10	AW661455 833006C11

ALIGNMENTS

RESULT 1	CE070440	178 bp	DNA	linear	GSS 24-SBP-2003
LOCUS	tigr-gss-dog-17000322997936	Dog Library	Canis familiaris	genomic,	
DEFINITION	Genomic survey sequence.				
ACCESSION	CE070440				
VERSION	CE070440.1	GI:35131550			
KEYWORDS	GSS.				
SOURCE	Canis familiaris (dog)				
ORGANISM	Canis familiaris				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
	1 (bases 1 to 178)				
	Kirschner,E.F., Hafna,V., Halpern,A.L., Levy,S., Remington,K.,				
	Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and				
	Venter,J.C.				
TITLE	The dog genome: survey sequencing and comparative analysis				
JOURNAL	Science 301 (5641), 1898-1903 (2003)				
MEDLINE	22875432				
PUBMED	14512627				
COMMENT	Contact: Kirkness EF				
	The Institute for Genomic Research				
	Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,				
	Rockville, MD 20850, USA				
	Tel: 301-838-0200				
	Fax: 301-838-0208				
	Email: ekirknes@tigr.org				

Tagu, D., Frey-Klett, P., Duplessis, S., Chalot, M., Podila, G. and Martin, P.
Analysis of expressed sequence tags from the ectomycorrhizal basidiomycetes *Laccaria bicolor* and *Pisolithus microcarpus* New Phytol. 159 (1), 117-129 (2003)
Contact: Martin FM
Equipe de Microbiologie Forestiere
Institut National de la Recherche Agronomique
Centre INRA de Nancy, 54280 Champenoux, France
Tel: +33 383 39 40 80
Fax: +33 383 39 40 69
Email: fmartin@nancy.inra.fr
Insert Length: 399 Std Error: 0.00
Seq primer: Fornat 5' AAGCGCGCATGTTGTGTGATACC.

Location/Qualifiers
1. 399
/organism="Laccaria bicolor"
/mol_type="mRNA"
/cultivar="5238N"
/db_xref="taxon:29883"
/dev_stage="ten-weeks-old"
/clone_lib="mycelium of Laccaria bicolor grown for ten weeks"
/note="Organ: mycelium; Vector: pTriplex2; Laccaria bicolor Maire Orton; cDNA library from mycelium of Laccaria bicolor grown for ten weeks on agar-plates containing low sugar (1 g/l glucose) Pachlewski medium. The cDNA library was constructed from mRNA which was isolated from 13ug of total Dnase digested RNA using the SMART cDNA synthesis kit (Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. The resulting cDNA was packed into lambda phages using the Gigapack III Gold packaging kit (Stratagene, La Jolla, CA). The pTriplex2 phagemid clones in Escherichia coli were obtained by using the mass in vivo excision protocol according to the manufacturer's instructions (Clontech)."

ORIGIN
Query Match 100.0%; Score 16; DB 14; Length 399;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16
|||||
Db 382 GGGCATGCATGGGGG 367

RESULT 5
AA798510/c
LOCUS
DEFINITION
vX68f08_r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
IMAGE:1280391 5', mRNA sequence.

ACCESSION
AA798510
VERSION
AA798510.1 GI:2861465
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)

ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 422)

REFERENCE
AUTHORS
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

THE WASHU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:672191
Seq primer: -28ml3 rev1 ET from Amersham.

Location/Qualifiers
1. 422
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1280391"
/sex="females"
/tissue type="whole skin"
/dev stage="11 weeks old"
/lab_hosts="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse skin (#937313)"
/note="Organ: skin; Vector: pBluescript SK-; Site: 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'"

ORIGIN
Query Match 100.0%; Score 16; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16
|||||
Db 377 GGGCATGCATGGGGG 362

RESULT 6
AA798509/c
LOCUS
DEFINITION
vX68f07_r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
IMAGE:1280389 5', mRNA sequence.

ACCESSION
AA798509
VERSION
AA798509.1 GI:2861464
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)

ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 423)

REFERENCE
AUTHORS
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

THE WASHU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:672189
Seq primer: -28ml3 rev1 ET from Amersham.

Location/Qualifiers
1. 423
/organism="Mus musculus"
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1280389"
/sex="females"

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/tissue type="whole skin"
/dev stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse skin (#937313)"
/note="Organ: skin; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN
Query Match 100.0%; Score 16; DB 9; Length 423;
Best Local Similarity 100.0%; Pred. NO. 3.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCATGCATGGGGG 16
Db 377 GGGCATGCATGGGGG 362

RESULT 7
BZ317770
LOCUS
DEFINITION hx35a03.g1 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays
ACCESSION BZ317770
VERSION BZ317770.1 GI:24689877
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 507)
Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N.,
Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: hx35 row: a column: 03
Seq primer: -21M3UnivRev
Class: shotgun
High quality sequence stop: 507.
Location/Qualifiers
1..507
/organism="Zea mays"
/mol_type="genomic DNA"
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/db_xref="taxon:4577"
/clone="hx35a03"
/lab_host="JM107 or DH5a"
/clone_lib="WGS-ZmaysF (JM107 adapted methyl filtered)"
/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(.x/y reads in M13mp19, .b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a."

ORIGIN
Query Match 100.0%; Score 16; DB 28; Length 507;
Best Local Similarity 100.0%; Pred. NO. 3.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCATGCATGGGGG 16
Db 137 GGGCATGCATGGGGG 122

RESULT 9
CNS07EQ7/c
LOCUS
DEFINITION Anopheles gambiae GSS T7 end of clone 02L03 of library NotreDame1
from strain PEST of Anopheles gambiae (African malaria mosquito),
genomic survey sequence.
ACCESSION AL607489
VERSION AL607489.1 GI:15913674
KEYWORDS GSS.

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Qy 1 GGGCATGCATGGGGG 16
Db 384 GGGCATGCATGGGGG 399

RESULT 8
BZ308462/c
LOCUS
DEFINITION id42f07.b1 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays
ACCESSION BZ308462
VERSION BZ308462.1 GI:24667742
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 525)
Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N.,
Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: id42 row: f column: 07
Seq primer: -21M13UnivPw
Class: shotgun
High quality sequence stop: 525.
Location/Qualifiers
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/mol_type="genomic DNA"
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/db_xref="taxon:4577"
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/lab_host="JM107 or DH5a"
/clone_lib="WGS-ZmaysF (JM107 adapted methyl filtered)"
/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(.x/y reads in M13mp19, .b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a."

ORIGIN
Query Match 100.0%; Score 16; DB 28; Length 525;
Best Local Similarity 100.0%; Pred. NO. 3.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCATGCATGGGGG 16
Db 137 GGGCATGCATGGGGG 122

RESULT 9
CNS07EQ7
LOCUS
DEFINITION Anopheles gambiae GSS T7 end of clone 02L03 of library NotreDame1
from strain PEST of Anopheles gambiae (African malaria mosquito),
genomic survey sequence.
ACCESSION AL607489
VERSION AL607489.1 GI:15913674
KEYWORDS GSS.

```

```

SOURCE
ORGANISM
Anopheles gambiae (African malaria mosquito)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.

REFERENCE
1 (bases 1 to 526)
Genoscope.

AUTHORS
Direct Submission

TITLE
Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage :
JOURNAL
BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

REFERENCE
2 (bases 1 to 526)
Roth,C.W., Brey,P.T., Ke,Z. and Collins,F.H.

AUTHORS
Direct Submission

TITLE
Submitted (01-OCT-2001) BWHI, Institut Pasteur, 25, rue du Dr.
JOURNAL
Roux, Paris 75015, France

COMMENT
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
Pasteur.

FEATURES
Location/Qualifiers
1..526
/organism="Anopheles gambiae"
/mol_type="genomic DNA"
/strain="PEST"
/db_xref="taxon:7165"
/clone="02103"
/clone_lib="NotreDame1"
/note="end : T7"

ORIGIN
Query Match 100.0%; Score 16; DB 29; Length 526;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCATGTCATGGGGGG 16
|||||
Db 225 GGGCATGTCATGGGGGG 210

RESULT 10
CE563190/c
LOCUS
DEFINITION
tigr-gss-dog-17000313666808 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION
CE563190
KEYWORDS
CE563190.1 GI:36982058
SOURCE
GSS.
ORGANISM
Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE
1 (bases 1 to 531)
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.

AUTHORS
The dog genome: survey sequencing and comparative analysis
TITLE
Science 301 (5641), 1898-1903 (2003)
JOURNAL
22875432
MEDLINE
14512627
PUBMED
Contact: Kirkness EF
COMMENT
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun
Location/Qualifiers
1..531
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"

FEATURES
source

```

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RESULT 12
BH877725
LOCUS
DEFINITION
hr54e02.g1 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays
genomic clone hr54e02 5', genomic survey sequence.
ACCESSION
BH877725
VERSION
BH877725.1 GI:22113622
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 577)
AUTHORS
Katzemburger, P., King, L., Miller, B., Muller, S., Nascimento, L.,
Zutavern, T., McCombie, W.R. and Martienssen, R.A.
Unpublished (2002)
TITLE
JOURNAL
COMMENT
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: hr54 row: e column: 02
Seq primer: -21M13UnivFwd
Class: shotgun
High quality sequence stop: 577.
FEATURES
source
Location/Qualifiers
1..577
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="hr54e02"
/lab_host="JM107 or DH5a"
/clone_lib="WGS-ZmaysF (JM107 adapted methyl filtered)"
/notes="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(X/Y reads in M13mpl9, b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a."
ORIGIN
Query Match 100.0%; Score 16; DB 28; Length 577;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCATGCATGGGGG 16
DB 547 GGGCATGCATGGGGG 562
RESULT 13
BZ308895
LOCUS
DEFINITION
BZ308895
1d76f05.b1 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays
genomic clone id76f05 5', genomic survey sequence.
ACCESSION
BZ308895
VERSION
BZ308895.1 GI:24669162
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 645)
AUTHORS
Rabinowicz, P.D., O'Shaughnessy, A.L., Ballija, V., Dedhia, N.,
Katzemburger, P., King, L., Miller, B., Muller, S., Nascimento, L.,
Zutavern, T., McCombie, W.R. and Martienssen, R.A.
Unpublished (2002)
TITLE
JOURNAL
COMMENT
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: id76 row: f column: 08
Seq primer: -21M13UnivFwd
Class: shotgun
High quality sequence stop: 667.

```

```

Katzemburger, P., King, L., Miller, B., Muller, S., Nascimento, L.,
Zutavern, T., McCombie, W.R. and Martienssen, R.A.
Unpublished (2002)
TITLE
JOURNAL
COMMENT
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: id76 row: f column: 05
Seq primer: -21M13UnivFwd
Class: shotgun
High quality sequence stop: 645.
FEATURES
source
Location/Qualifiers
1..645
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="id76f05"
/lab_host="JM107 or DH5a"
/clone_lib="WGS-ZmaysF (JM107 adapted methyl filtered)"
/notes="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(X/Y reads in M13mpl9, b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a."
ORIGIN
Query Match 100.0%; Score 16; DB 28; Length 645;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCATGCATGGGGG 16
DB 470 GGGCATGCATGGGGG 485
RESULT 14
BZ371261/c
LOCUS
DEFINITION
BZ371261
ie33b08.b1 WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone
ie33b08 5', genomic survey sequence.
ACCESSION
BZ371261.1 GI:25455161
VERSION
BZ371261
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 667)
AUTHORS
Rabinowicz, P.D., O'Shaughnessy, A.L., Ballija, V., Dedhia, N.,
Katzemburger, P., King, L., Miller, B., Muller, S., Nascimento, L.,
Zutavern, T., McCombie, W.R. and Martienssen, R.A.
Unpublished (2002)
TITLE
JOURNAL
COMMENT
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: ie33 row: b column: 08
Seq primer: -21M13UnivFwd
Class: shotgun
High quality sequence stop: 667.

```

FEATURES

source

Location/Qualifiers
1. -667
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ie33b08"
/lab_host="DH5a"
/clone_lib="WGS-ZmaysP (DH5a methyl filtered)"
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector (.x/y
reads in M13mpl9, .b/g reads in pUC19). The same ligation
was transformed into DH5a."

ORIGIN

Query Match 100.0%; Score 16; DB 28; Length 667;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16
Db 97 GGGCATGCATGGGGG 82

RESULT 15

BZ413880
LOCUS BZ413880 673 bp DNA linear GSS 10-DEC-2002
DEFINITION if18e05.g1 WGS-ZmaysP (DH5a methyl filtered) Zea mays genomic clone
if18e05.5', genomic survey sequence.
ACCESSION BZ413880
VERSION BZ413880.1 GI:26355896
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 673)
Rabinowicz,P.D., O'Shaughnessy,A.L., Balijs,V., Dedhia,N.,
Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: if18 row: e column: 05
Seq primer: -21M13UnivRev
Class: shotgun
High quality sequence stop: 673.

FEATURES

source

Location/Qualifiers
1. -673
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="if18e05"
/lab_host="DH5a"
/clone_lib="WGS-ZmaysP (DH5a methyl filtered)"
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector (.x/y

reads in M13mpl9, .b/g reads in pUC19). The same ligation
was transformed into DH5a."

ORIGIN

Query Match 100.0%; Score 16; DB 28; Length 673;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCATGCATGGGGG 16
Db 68 GGGCATGCATGGGGG 83

Search completed: July 2, 2004, 13:32:59
Job time : 1201.35 secs

; Sequence 119, Application US/10194035
; Publication No. US2003014229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 119
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-119

Query Match 100.0%; Score 16; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16
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DB 1 GGGCATGCATGGGGG 16

RESULT 3
US-09-802-668-47/c
; Sequence 47, Application US/09802668
; Publication No. US20030190714A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Linda
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Karnovsky, Alla
; APPLICANT: Linske-O'Connell, Lisa I.
; APPLICANT: Wang, Jun
; APPLICANT: Liu, Derong
; TITLE OF INVENTION: Human Ion Channels
; FILE REFERENCE: 00069US1
; CURRENT APPLICATION NUMBER: US/09/802,668
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,517
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 47
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-802-668-47

Query Match 93.8%; Score 15; DB 10; Length 657;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 15
|||||
DB 550 GGGCATGCATGGGGG 536

RESULT 4
US-10-243-475-47/c
; Sequence 47, Application US/10243475
; Publication No. US20030194720A1

; GENERAL INFORMATION:
; APPLICANT: Roberts, Steven L.
; APPLICANT: Benjamin, Christopher W.
; APPLICANT: Karnovsky, Alla M.
; APPLICANT: Ruble, Cara L.
; TITLE OF INVENTION: Human Ion Channels
; FILE REFERENCE: PHEM0039-100
; CURRENT APPLICATION NUMBER: US/10/243,475
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 60/403,254
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 60/318,733
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 47
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-243-475-47

Query Match 93.8%; Score 15; DB 15; Length 657;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 15
|||||
DB 550 GGGCATGCATGGGGG 536

RESULT 5
US-10-087-192-2017/c
; Sequence 2017, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2017
; LENGTH: 82660
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1)..(82660)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-2017

Query Match 93.8%; Score 15; DB 13; Length 82660;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 15
|||||
DB 49515 GGGCATGCATGGGGG 49501

RESULT 6
US-10-437-963-34086/c
; Sequence 34086, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 34086
 ; LENGTH: 388
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_38135C.1
 US-10-437-963-34086

Query Match 90.0%; Score 14.4; DB 17; Length 388;
 Best Local Similarity 93.8%; Pred. No. 6.5e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCGTGGGGG 16
 |||||
 DB 124 GGGCATGCGTGGGGG 109

RESULT 7
 US-09-867-701-1577
 ; Sequence 1577, Application US/09867701
 ; Patent No. US2002013237A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aglate, Paul A.
 ; APPLICANT: Jones, Robert
 ; APPLICANT: Harlocker, Susan L.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.497
 ; CURRENT APPLICATION NUMBER: US/09/867,701
 ; CURRENT FILING DATE: 2001-05-29
 ; NUMBER OF SEQ ID NOS: 10912
 ; SOFTWARE: PastSeq for Windows Version 4.0
 ; SEQ ID NO 1577
 ; LENGTH: 390
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1)...(390)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-867-701-1577

Query Match 90.0%; Score 14.4; DB 9; Length 390;
 Best Local Similarity 93.8%; Pred. No. 6.5e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCGTGGGGG 16
 |||||
 DB 229 GGGCATGCGTGGGGG 244

RESULT 8
 US-09-918-995-6563/c
 ; Sequence 6563, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/918,995
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076
 ; PRIOR FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 6563
 ; LENGTH: 462
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1)...(462)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-6563

Query Match 90.0%; Score 14.4; DB 10; Length 462;
 Best Local Similarity 93.8%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCGTGGGGG 16
 |||||
 DB 275 GGGCATGCGTGGGGG 260

RESULT 9
 US-09-918-995-21067/c
 ; Sequence 21067, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918,995
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076
 ; PRIOR FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 21067
 ; LENGTH: 475
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-918-995-21067

Query Match 90.0%; Score 14.4; DB 10; Length 475;
 Best Local Similarity 93.8%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCGTGGGGG 16
 |||||
 DB 340 GGGCATGCGTGGGGG 325

RESULT 10
 US-10-029-386-12515/c
 ; Sequence 12515, Application US/10029386
 ; Publication No. US20030194704A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
 ; FILE REFERENCE: ASOMICA-X-2
 ; CURRENT APPLICATION NUMBER: US/10/029,386
 ; CURRENT FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 34288
 ; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 12515
 ; LENGTH: 518
 ; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3
; OTHER INFORMATION: SWISSPROT HIT: P09012, EVALUE 1.00e-09
; OTHER INFORMATION: NT_HIT: M60784.1, EVALUE 1.00e-111
; OTHER INFORMATION: EST_HUMAN_HIT: MS18377.1, EVALUE 1.00e-85
US-10-029-386-12515

Query Match          90.0%; Score 14.4; DB 15; Length 518;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCATGCGTGGGGG 16
   ||||| ||||| |||||
Db 119 GGCAGCGCATGGGGG 104

RESULT 11
US-10-027-632-142400
; Sequence 142400, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/136,358
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142400
; LENGTH: 607
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; ORGANISM: Human
US-10-027-632-142400

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Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCATGCGTGGGGG 16
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; Sequence 142401, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
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; PRIOR FILING DATE: 1999-08-09
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US-10-027-632-142400

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US-10-027-632-142400
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; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
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US-10-027-632-142400

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Db 403 GAGCATGCGTGGGGG 418
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; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
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; PRIOR FILING DATE: 2000-02-24
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US-10-027-632-142401

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Best Local Similarity 93.8%; Pred. No. 6.2e+02;
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DB 403 GAGCATGCATGGGGG 418

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; Sequence 22690, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
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; OTHER INFORMATION: unsure at all n locations
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US-10-437-963-22690

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Job time : 123.317 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:36:05 ; Search time 633.732 Seconds
(without alignments)
1231.080 Million cell updates/sec

Title: US-10-068-160-16

Perfect score: 18
Sequence: 1 tgcgtcgatgcagggggg 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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2	18	100.0	20	6	AX194481	AX194481 Sequence
3	18	100.0	20	6	AX194482	AX194482 Sequence
4	18	100.0	20	6	AX465390	AX465390 Sequence
5	18	100.0	20	6	AX465431	AX465431 Sequence
6	18	100.0	20	6	AX465432	AX465432 Sequence
7	17	94.4	19	6	AX194483	AX194483 Sequence
8	17	94.4	19	6	AX465433	AX465433 Sequence
9	16.4	91.1	18	6	AX352207	AX352207 Sequence
10	16.4	91.1	18	6	AX352217	AX352217 Sequence
11	16.4	91.1	18	6	AX352255	AX352255 Sequence
12	16.4	91.1	20	6	AX194432	AX194432 Sequence
13	16.4	91.1	20	6	AX194434	AX194434 Sequence
14	16.4	91.1	20	6	AX194437	AX194437 Sequence
15	16.4	91.1	20	6	AX194438	AX194438 Sequence
16	16.4	91.1	20	6	AX194439	AX194439 Sequence
17	16.4	91.1	20	6	AX194441	AX194441 Sequence
18	16.4	91.1	20	6	AX194443	AX194443 Sequence
19	16.4	91.1	20	6	AX194472	AX194472 Sequence
20	16.4	91.1	20	6	AX194502	AX194502 Sequence
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22	16.4	91.1	20	6	AX352201	AX352201 Sequence
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24	16.4	91.1	20	6	AX352209	AX352209 Sequence
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26	16.4	91.1	20	6	AX352216	AX352216 Sequence
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ALIGNMENTS

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ACCESSION	AX194440	AX194440	Sequence	40 from Patent WO0151500.	20 bp	DNA	linear	PAT 28-AUG-2001
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ORGANISM	AX194440.1	AX194440.1	GI:15385096	GI:15385096	20 bp	DNA	linear	PAT 28-AUG-2001
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1
Kliman, D., Ishii, K. and Verthelyi, D.
Oligodeoxynucleotide and its use to induce an immune response
Patent: WO 0151500-A 40 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)

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  REFERENCE
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  AUTHORS
    Kliman, D., Ishii, K. and Verthelyi, D.
  TITLE
    Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL
    Patent: WO 0151500-A 81 19-JUL-2001;
    Secretary of the Department of Health and Human Services (US)
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  VERSION
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    Kliman, D., Ishii, K. and Verthelyi, D.
  TITLE
    Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL
    Patent: WO 0151500-A 82 19-JUL-2001;
    Secretary of the Department of Health and Human Services (US)
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  AUTHORS
    Mond, J.J., Prince, G. and Klinman, D.M.
  TITLE
    Vaccine against RSV
  JOURNAL
    Patent: WO 0211761-A 58 14-FEB-2002;
    HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
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  JOURNAL
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ACCESSION AX465432
VERSION AX465432.1 GI:21899795
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mond,J.J., Prince,G. and Klinman,D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 100 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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Location/Qualifiers
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DEFINITION Sequence 83 from Patent WO0151500.
ACCESSION AX194483
VERSION AX194483.1 GI:15385139
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 83 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
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RESULT 8
LOCUS AX465433 19 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 101 from Patent WO0211761.
ACCESSION AX465433
VERSION AX465433.1 GI:21899796
KEYWORDS

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SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mond,J.J., Prince,G. and Klinman,D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 101 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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DEFINITION Sequence 503 from Patent WO0193902.
ACCESSION AX352207
VERSION AX352207.1 GI:18617490
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mond,J.J., Flora,M. and Klinman,D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 503 13-DEC-2001;
Biosynexus Incorporated (US)
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DEFINITION Sequence 513 from Patent WO0193902.
ACCESSION AX352217
VERSION AX352217.1 GI:18617500
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mond,J.J., Flora,M. and Klinman,D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 513 13-DEC-2001;
Biosynexus Incorporated (US)

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RESULT 13

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VERSION	AX194434.1	GI:15385090			
KEYWORDS					

REFERENCE	1	Kliman,D., Ishii,K. and Verthelyi,D. Oligodeoxynucleotide and its use to induce an immune response Patent: WO 0151500-A 34 19-JUL-2001;
AUTHORS		Secretary of the Department of Health and Human Services (US)
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	DNA	linear
		PAT 28-AUG-2001

DEFINITION
SEQUENCE 37 FROM PATENT #00131306.
ACCESSION
AXI194437
VERSION
AXI194437.1 GI:15385093
KEYWORDS

```

ORGANISM
1
REFERENCE
1
AUTHORS
Klimman,D., Ishii,K. and Verthelyi,D.
TITLE
Oligodeoxynucleotide and its use to induce an immune response
JOURNAL
Patent: WO 0151500-A 37 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
FEATURES
Location/Qualifiers
1..20
/molecule="synthetic construct"
/mol_type="unassigned DNA"

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ORIGIN
      91.1%; Score 16.4; DB 6; Length 20;
Best Match
Query Local Similarity 94.4%; Pred. No. 1 6e+03;
/cw_xref="taxon:32630-
/note="Synthetic DNA"

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	matches	17; Conservative	0; mismatches	1; indels	0; gaps
Qy	1	TCGTCGATCGACGGGGG	18		
Db	3	TGCATCGATCGACGGGGG	20		

RESULT 15

AX194438
LOCUS AX194438 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 38 from Patent WO0151500.
ACCESSION AX194438
VERSION AX194438.1 GI:15385094
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Klinman,D., Ishii,K. and Verthelyi,D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 38 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
FEATURES
Source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA"
ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Fred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TCGCTCGATGCAGGGGG 18
||| |||||
Db 3 TGCATCGATGCAGGGGG 20
Search completed: July 2, 2004, 10:08:03
Job time : 633.732 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:38:45 ; Search time 1348.02 Seconds
(without alignments)
398.746 Million cell updates/sec

Title: US-10-068-160-16

Perfect score: 18

Sequence: 1 tgcgtcgatcagggggggg 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_estlin:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	94.4	1026	11	CNS08MNL
2	16.4	91.1	360	9	AA056330
3	16.4	91.1	429	28	BH746584
4	16.4	91.1	1110	29	AG082246

5	16	88.9	489	13	BQ102588
6	16	88.9	705	29	CE730492
7	15.6	86.7	893	13	BA448966
8	15.4	85.6	125	9	AV128107
9	15.4	85.6	320	9	AA662789
10	15.4	85.6	366	10	BA400545
11	15.4	85.6	442	14	CA706144
12	15.4	85.6	470	14	CA693337
13	15.4	85.6	499	9	AU001427
14	15.4	85.6	553	14	CF639409
15	15.4	85.6	565	28	BH797911
16	15.4	85.6	590	12	BJ232664
17	15.4	85.6	621	9	AV398828
18	15.4	85.6	633	14	CA760384
19	15.4	85.6	653	14	CF642132
20	15.4	85.6	720	9	AV401323
21	15.4	85.6	742	12	BG707792
22	15.4	85.6	749	29	AG100828
23	15.4	85.6	759	9	AU002700
24	15.4	85.6	781	29	AG042213
25	15.4	85.6	802	28	BH983112
26	15.4	85.6	807	13	CA101677
27	15.4	85.6	808	10	BF530495
28	15.4	85.6	870	29	CG254815
29	15.4	85.6	877	29	CG238619
30	15.4	85.6	907	29	CG62082
31	15.4	85.6	929	29	CG254827
32	15.4	85.6	931	9	AU091129
33	15.4	85.6	955	10	BF794250
34	15.4	85.6	964	29	CG662091
35	15.4	85.6	972	29	CG615817
36	15.4	85.6	1015	29	CNS054D6
37	15.4	85.6	1055	10	BB869694
38	15.4	85.6	1064	12	BG920455
39	15.4	85.6	1071	13	BJ253418
40	15.4	85.6	1390	13	BQ877978
41	15	83.3	448	29	CG740971
42	15	83.3	449	9	AU173854
43	15	83.3	958	12	BI758635
44	15	83.3	1015	9	AV117227
45	15	83.3	1399	28	BZ579332

ALIGNMENTS

RESULT 1	CNS08MNL	1026 bp	mRNA	linear	HTC 07-JAN-2003
LOCUS	Single read from an extremity of a full-length cDNA clone made from Anopheles gambiae total adult females. 3-PRIME end of clone PK0AA28CA12 of strain 6-9 of Anopheles gambiae (African malaria mosquito).				
DEFINITION	Single read from an extremity of a full-length cDNA clone made from Anopheles gambiae total adult females. 3-PRIME end of clone PK0AA28CA12 of strain 6-9 of Anopheles gambiae (African malaria mosquito).				
ACCESSION	BX018781				
VERSION	BX018781.1 GI:27568001				
KEYWORDS	HTC.				
SOURCE	Anopheles gambiae (African malaria mosquito)				
ORGANISM	Anopheles gambiae				
REFERENCE	1 (bases 1 to 1026)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)				
FEATURES	Location/Qualifiers				
Source	1..1026				
	/organism="Anopheles gambiae"				
	/mol_type="mRNA"				
	/strain="6-9"				
	/db_xref="taxon:7165"				

/clone="FK0AAA28CA12"
/plasmid="pME18S-FL"
/note="end : 3-PRIME"

ORIGIN

Query Match 94.4%; Score 17; DB 11; Length 1026;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGATCGAGGGGG 18
|||||
Db 205 GCGTCGATCGAGGGGG 221

RESULT 2

AA066330

LOCUS

DEFINITION

mm14606.r1 Stragene mouse diaphragm (#937303) Mus musculus cDNA
clone IMAGE:521506 5' similar to gb:X03208 Mouse group 1 gene
(MOUSE); mRNA sequence.

ACCESSION

AA066330

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..360

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:521506"

/issue_type="diaphragm"

/dev_stage="adult"

/lab_host="SOLR (kanamycin resistant)"

/clone_lib="Stragene mouse diaphragm (#937303)"

/note="Organ: diaphragm; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally from mRNA
prepared from diaphragm muscle. Primer: Oligo dt. Average
insert size: 1.5 kb. Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5'
CTCGAGTTTCTTTTCTTTT 3'"

Query Match

Best Local Similarity

Matches

17; Conservative

0; Mismatches

1; Indels

0; Gaps

0;

QY

1

TGCCTCGATCGAGGGGG 18

|||||

Db

91

TGTGTCGATCGAGGGGG 109

ORIGIN

Query Match 91.1%; Score 16.4; DB 9; Length 360;
Best Local Similarity 94.4%; Pred. No. 6.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCTCGATCGAGGGGG 18

|||||

Db 91 TGTGTCGATCGAGGGGG 109

RESULT 3

BH746584/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..429

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_044872.30.00.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

Query Match

Best Local Similarity

Matches

17; Conservative

0; Mismatches

1; Indels

0; Gaps

0;

QY

1

TGCCTCGATCGAGGGGG 18

|||||

Db

414

TGCCTCGATCGAGGGGG 397

|||||

RESULT 4

AG082246/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..1110

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_044872.30.00.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

Query Match

Best Local Similarity

Matches

17; Conservative

0; Mismatches

1; Indels

0; Gaps

0;

QY

1

TGCCTCGATCGAGGGGG 18

|||||

Db

91

TGTGTCGATCGAGGGGG 109

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JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
ORIGIN
Query Match      88.9%; Score 16; DB 13; Length 489;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGTCGATCGACGGGG 18
    |||||
Db 143 CGTCGATCGACGGGG 158
    |||||

RESULT 6
LOCUS CE730492/c
DEFINITION tigr-gss-dog-17000315416995 Dog Library Canis familiaris genomic,
          genomic survey sequence.
ACCESSION CE730492
VERSION CE730492.1 GI:37070612
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE 1 (bases 1 to 705)
AUTHORS Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
          Kirkness,E.F., Baina,V., Halpern,A.L., Levy,S., Remington,K.,
          Rusch,D.B., Delcher,A.L., Pop.M., Wang,W., Fraser,C.M. and
          Venter,J.C.
          The dog genome: survey sequencing and comparative analysis
          Science 301 (5641), 1898-1903 (2003)
          22875432
          PUBLISHED 14512627
COMMENT Contact: Kirkness EP
          The Institute for Genomic Research
          Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
          Rockville, MD 20850, USA
          Tel: 301-838-0200
          Fax: 301-838-0208
          Email: ekirknes@tigr.org
          Class: shotgun.
          Location/Qualifiers
            1..705
              /organism="Canis familiaris"
              /mol_type="genomic DNA"
              /strain="Standard poodle"
              /db_xref="taxon:9615"
              /clone_lib="dog Library"
              /note="Site 1: BstXI; Libraries were prepared from
              peripheral blood"

FEATURES
source
LOCUS CE730492/c
DEFINITION tigr-gss-dog-17000315416995 Dog Library Canis familiaris genomic,
          genomic survey sequence.
ACCESSION CE730492
VERSION CE730492.1 GI:37070612
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE 1 (bases 1 to 705)
AUTHORS Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
          Kirkness,E.F., Baina,V., Halpern,A.L., Levy,S., Remington,K.,
          Rusch,D.B., Delcher,A.L., Pop.M., Wang,W., Fraser,C.M. and
          Venter,J.C.
          The dog genome: survey sequencing and comparative analysis
          Science 301 (5641), 1898-1903 (2003)
          22875432
          PUBLISHED 14512627
COMMENT Contact: Kirkness EP
          The Institute for Genomic Research
          Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
          Rockville, MD 20850, USA
          Tel: 301-838-0200
          Fax: 301-838-0208
          Email: ekirknes@tigr.org
          Class: shotgun.
          Location/Qualifiers
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              /organism="Canis familiaris"
              /mol_type="genomic DNA"
              /strain="Standard poodle"
              /db_xref="taxon:9615"
              /clone_lib="dog Library"
              /note="Site 1: BstXI; Libraries were prepared from
              peripheral blood"

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
ORIGIN
Query Match      88.9%; Score 16; DB 29; Length 705;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTCGATCGACGGGG 16
    |||||
Db 297 TCGTCGATCGACGGGG 282
    |||||

RESULT 7
LOCUS BX448966
DEFINITION BX448966 Homo sapiens FETAL LIVER Homo sapiens CDNA clone
          CSODM012YN11 5-PRIME, mRNA sequence.
ACCESSION BX448966
VERSION BX448966.1 GI:31035980
KEYWORDS EST.

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
ORIGIN
Query Match      88.9%; Score 16; DB 29; Length 705;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTCGATCGACGGGG 16
    |||||
Db 297 TCGTCGATCGACGGGG 282
    |||||

RESULT 7
LOCUS BX448966
DEFINITION BX448966 Homo sapiens FETAL LIVER Homo sapiens CDNA clone
          CSODM012YN11 5-PRIME, mRNA sequence.
ACCESSION BX448966
VERSION BX448966.1 GI:31035980
KEYWORDS EST.

```

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 893)
 AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. Contact : Peng Liang Email :
 fliang@lifetech.com URL : http://fulllength.invitrogen.com/
 Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID :
 CS0AM012CG06QPL.

FEATURES source
 Location/Qualifiers
 1..893
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0AM012YNI1"
 /tissue_type="FETAL LIVER"
 /dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL LIVER"
 /note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with NotI and
 cloned into the NotI and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN
 Query Match 86.7%; Score 15.6; DB 13; Length 893;
 Best Local Similarity 93.8%; Pred. No. 1.7e+04;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGATCGAGGGG 17
 |||||
 Db 59 GCGTCGATCGAGGGG 74

RESULT 8
 AV128107 125 bp mRNA linear EST 01-JUL-1999
 LOCUS AV128107 Mus musculus C57BL/6J 11-day embryo Mus musculus cDNA
 DEFINITION Clone 2700054B15, mRNA sequence.

ACCESSION AV128107 GI:5314341
 VERSION AV128107
 KEYWORDS EST
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 125)
 AUTHORS Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
 Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T.,
 Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M.,
 Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Naitsuma, H., Oda, H.,
 Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y.,
 Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y.,
 Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T.,
 Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 RIKEN Mouse ESTs
 Unpublished (1999)
 CONTACT Chie Owa
 Genomic Science Laboratory
 RIKEN

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
 Fax: 81-298-36-9098
 Email: genome-res@rtc.riken.go.jp
 Thermotabilization and thermostabilization of thermolabile enzymes by

trehalose and its application for the synthesis of full length cDNA
 (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

FEATURES source
 Location/Qualifiers
 1..125
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="2700054B15"
 /sex="mixed"
 /dev_stage="11-day embryo"
 /clone_lib="Mus musculus C57BL/6J 11-day embryo"

ORIGIN
 Query Match 85.6%; Score 15.4; DB 9; Length 125;
 Best Local Similarity 94.1%; Pred. No. 1.4e+04;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGTCGATCGAGGGG 18
 |||||
 Db 15 GCGTCGATCGAGGGG 31

RESULT 9
 AA662789 320 bp mRNA linear EST 12-NOV-1997
 LOCUS AA662789.1 NCI CGAP Pr22 Homo sapiens cDNA clone IMAGE:1218808 3;
 DEFINITION similar to gb:XI2794_cds1 V-ERBA RELATED PROTEIN EAR-2 (HUMAN);
 mRNA sequence.

ACCESSION AA662789 GI:2616780
 VERSION AA662789.1
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 320)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES source
 1..320
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1218808"
 /sex="male"
 /tissue_type="normal prostate"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Pr22"
 /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
 with a modified polylinker; 1st strand cDNA was prepared
 from normal prostate bulk tissue, and was then primed with
 a Not I - oligo(dT) primer. Double-stranded cDNA was

ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Donaldo. "

ORIGIN

Query Match 85.6%; Score 15.4; DB 9; Length 320;
Best Local Similarity 94.1%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGTCGATGCAGGGGGG 18
Db 68 GCGCCGATGCAGGGGGG 52

RESULT 10

BE400545/c
LOCUS
DEFINITION BE400545 366 bp mRNA linear EST 21-JUL-2000
aestivum cDNA clone AWB004.G12, mRNA sequence.

ACCESSION BE400545
VERSION
KEYWORDS
SOURCE
ORGANISM

Triticum aestivum (bread wheat)

REFERENCE
AUTHORS Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemelin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M., and Wenzel, G.
TITLE International Triticaceae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticaceae
JOURNAL Unpublished (2000)
COMMENT Contact: Langridge P
Special Research Centre, Basic and Applied Plant Molecular Biology
Waite Campus, University of Adelaide, Glen Osmond SA 5064 AUSTRALIA
Tel: 61 8 8303 7368
Fax: 61 8 8303 7102
Email: plangridge@waite.adelaide.edu.au
International Triticaceae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.

FEATURES

Location/Qualifiers

1..366

/organism="Triticum aestivum"

/mol_type="mRNA"

/cultivar="Chinese Spring"

/db_xref="taxon:4565"

/clone="AWB004.G12"

/tissue_type="excised florets"

/dev_stage="meiotic stage no later than metaphase I"

/clone_lib="ITEC AWS Wheat Meiotic Stage Library"

/notes="Vector: pSport 1 (Life Technologies cat. no. 18248-013); Site 1: SalI; Library constructed in pSport 1. Directionally cloned using the Superscript Plasmid System for cDNA synthesis and plasmid cloning. M13 Reverse sequencing primer used to obtain 5' sequence data. 1.4 kbp average insert size."

1..366

/organism="Triticum aestivum"

/mol_type="mRNA"

/cultivar="Chinese Spring"

/db_xref="taxon:4565"

/clone="AWB004.G12"

/tissue_type="excised florets"

/dev_stage="meiotic stage no later than metaphase I"

/clone_lib="ITEC AWS Wheat Meiotic Stage Library"

/notes="Vector: pSport 1 (Life Technologies cat. no. 18248-013); Site 1: SalI; Library constructed in pSport 1. Directionally cloned using the Superscript Plasmid System for cDNA synthesis and plasmid cloning. M13 Reverse sequencing primer used to obtain 5' sequence data. 1.4 kbp average insert size."

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1..366

/organism="Triticum aest

FEATURES source location/Qualifiers

1..470
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Stephens"
/db_xref="taxon:4565"
/clone="wlm96.pk061.b18"
/tissue_type="leaf"
/clone_lib="wlm96"
/note="Vector: pluscript SK+, Site 1: EcoRI; Site 2: XhoI; Wheat (Triticum aestivum L.) seedlings 96 hr after inoculation w/ E. graminis"

ORIGIN

Query Match 85.6%; Score 15.4; DB 14; Length 470;
Best Local Similarity 94.1%; Pred. No. 1.8e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGTCGATCGAGGGGG 18
|||||

Db 136 GCGTCGATCGAGGGGG 120
|||||

RESULT 13
AU001427
LOCUS
DEFINITION AU001427 Bombyx mori p50(Daizo) Bombyx mori cDNA clone fbm0407f, mRNA sequence.
ACCESSION AU001427 GI:4157671
VERSION AU001427.1
KEYWORDS EST.
SOURCE Bombyx mori (domestic silkworm)
ORGANISM Bombyx mori
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.
REFERENCE 1 (bases 1 to 499)
Mita K, Morimyo M., Shimada T., Okano K. and Maeda S.
TITLE Establishment of cDNA database of Bombyx mori
JOURNAL Unpublished (1999)
COMMENT Contact: Mita K
Genome Research Group
National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Email: kmita@nias.affrc.go.jp
PROJECT = CREST project by JST.
LOCATION/Qualifiers
1..499
/organism="Bombyx mori"
/mol_type="mRNA"
/strain="p50(Daizo)"
/db_xref="taxon:7091"
/clone="fbm0407f"
/clone_lib="Bombyx mori p50(Daizo)"

ORIGIN

Query Match 85.6%; Score 15.4; DB 9; Length 499;
Best Local Similarity 94.1%; Pred. No. 1.8e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGTCGATCGAGGGGG 18
|||||

Db 411 GCGTCGATCGAGGGGG 427
|||||

RESULT 14
CF639409
LOCUS
DEFINITION CF639409 553 bp mRNA linear EST 02-OCT-2003 D15_D01 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA sequence.
ACCESSION CF639409
VERSION CF639409
KEYWORDS EST.
EST. CF639409.1 GI:37403984

SOURCE Ustilago maydis
ORGANISM Ustilago maydis
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes; Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
REFERENCE 1 (bases 1 to 553)
Nugent K.G., Choffe K. and Saville B.J.
AUTHORS Gene Expression during Ustilago maydis Diploid Filamentous Growth: EST Library Creation and Analyses
TITLE EST Library Creation and Analyses
JOURNAL Unpublished (2003)
COMMENT Contact: Barry J. Saville
Saville Lab
University of Toronto
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Fax: 905 828 3792
Email: bsaville@utoronto.ca
Plate: UTM-UM-D126/7-015-UTM row: 01 column: D
Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGG 3')
High quality sequence stop: 553.
Location/Qualifiers
1..553
/organism="Ustilago maydis"
/mol_type="mRNA"
/strain="FBD12"
/db_xref="taxon:5270"
/cell_type="Mycelia"
/dev_stage="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"
/note="Vector: pSPORT; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

ORIGIN

Query Match 85.6%; Score 15.4; DB 14; Length 553;
Best Local Similarity 94.1%; Pred. No. 1.8e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGATCGAGGGGG 17
|||||

Db 226 TCGTCGATCGAGGGG 242
|||||

RESULT 15
BH797911
LOCUS
DEFINITION BH797911 565 bp DNA linear GSS 25-APR-2002 1008096D04.xl 1008 - RescueMu Grid I Zea mays genomic, genomic survey sequence.
ACCESSION BH797911 GI:20307382
VERSION BH797911.1
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 565)
Walbot V.
AUTHORS Maize genomic sequences found using engineered RescueMu transposon
TITLE Unpublished (2001)
JOURNAL Contact: Walbot V
COMMENT Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation sequence submitted separately.
Plate: 1008096 row: 26
Class: transposon-tagged.
Location/Qualifiers
1..565

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/Al88/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1008 - RescueMu Grid I"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 Kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site www.zmdb.iastate.edu and follow the links for
'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

ORIGIN

Query Match 85.6%; Score 15.4; DB 28; Length 565;
Best Local Similarity 94.1%; Pred. No. 1.8e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGATCGAGGGG 17
||| |||||
Db 521 TCGCGGATCGAGGGG 537

Search completed: July 2, 2004, 13:33:02
Job time : 1351.14 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 06:05:50 ; Search time 134.89 Seconds

(without alignments)
566.887 Million cell updates/sec

Title: US-10-068-160-16

Perfect score: 18

Sequence: 1 tgcgtcgatgcagggggg 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002s.*

7: Geneseqn2003as.*

8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	18	100.0	20	4	AAC80662 Immunogen
2	18	100.0	20	4	AAC80661 Immunogen
3	18	100.0	20	4	AAC80620 Immunogen
4	18	100.0	20	4	AAS09631 Immunorea
5	18	100.0	20	4	AAS09590 Immunorea
6	18	100.0	20	4	AAS09632 Immunorea
7	18	100.0	20	6	ABL35586 Immunosti
8	18	100.0	20	6	ABL35587 Immunosti
9	18	100.0	20	6	ABL35588 Immunosti
10	18	100.0	20	7	ACC48298 Cpg oligo
11	18	100.0	20	7	ACC48312 Cpg oligo
12	18	100.0	20	7	ACC48306 Cpg oligo
13	18	100.0	20	7	ACC48319 Cpg oligo
14	18	100.0	20	8	ACC83117 D class C
15	18	100.0	20	8	ACC83124 D class C
16	18	100.0	20	9	ADD01050 Cpg D oli
17	17	94.4	19	4	AAC80663 Immunogen
18	17	94.4	19	4	AAS09633 Immunorea
19	17	94.4	19	6	ABL35587 Immunosti
20	16.4	91.1	18	6	ABL35588 Immunosti
21	16.4	91.1	18	6	ABL35577 Immunosti
22	16.4	91.1	18	6	ABL35625 Immunosti
23	16.4	91.1	18	9	ADD01052 Cpg D oli

24	16.4	91.1	20	4	AAC80619	Immunogen
25	16.4	91.1	20	4	AAC80621	Immunogen
26	16.4	91.1	20	4	AAC80652	Immunogen
27	16.4	91.1	20	4	AAC80614	Immunogen
28	16.4	91.1	20	4	AAC80612	Immunogen
29	16.4	91.1	20	4	AAC80617	Immunogen
30	16.4	91.1	20	4	AAC80618	Immunogen
31	16.4	91.1	20	4	AAC80623	Immunogen
32	16.4	91.1	20	4	AAS09622	Immunorea
33	16.4	91.1	20	4	AAS09591	Immunorea
34	16.4	91.1	20	4	AAS09582	Immunorea
35	16.4	91.1	20	4	AAS09587	Immunorea
36	16.4	91.1	20	4	AAS09589	Immunorea
37	16.4	91.1	20	4	AAS09593	Immunorea
38	16.4	91.1	20	4	AAS09584	Immunorea
39	16.4	91.1	20	4	AAS09652	Immunorea
40	16.4	91.1	20	4	AAS09588	Immunorea
41	16.4	91.1	20	6	ABL35576	Immunosti
42	16.4	91.1	20	6	ABL35582	Immunosti
43	16.4	91.1	20	6	ABL35586	Immunosti
44	16.4	91.1	20	6	ABL35568	Immunosti
45	16.4	91.1	20	6	ABL35624	Immunosti

ALIGNMENTS

RESULT 1

ID AAC80662 standard; DNA; 20 BP.

AC AAC80662;

DT 14-FEB-2001 (first entry)

DE Immunogenic Cpg oligodeoxynucleotide, SEQ ID NO:82.

Cpg oligodeoxynucleotide; unmethylated; antigen-presenting cell; immunogenic; cytokine release; natural killer cell; NK cell activation; cell-mediated immune response; T-cell response; humoral response; B-cell response; antibody production; immune response induction; vaccine; allergy; asthma; infection; bacterial; viral; fungal; protozoal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer; immune deficiency; biological warfare agent; cytostatic; antiarthritic; antimicrobial; antiallergic; protozoacide; tuberculostatic; antiasthmatic; dermatological; phosphorothioate; ss.

OS Synthetic.

XX WO200061151-A2.

XX 19-OCT-2000.

XX 12-APR-2000; 2000WO-US009839.

XX 12-APR-1999; 99US-0128898P.

XX (KLIN/) KLINMAN D.

XX (ISHI/) ISHII K.

XX (VERT/) VERTHELXI D.

XX Klinman D, Ishii K, Verthelyi D;

XX WPI; 2001-006880/01.

XX Novel oligonucleotides useful for the prevention and treatment of

PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms

PT resulting from exposure to a bio-warfare agent.

XX Claim 4; Page 36; 46pp; English.

XX The invention relates to novel immunogenic Cpg oligodeoxynucleotides

CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
 CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
 CC optionally have phosphorothioate linkages which make them more resistant
 CC to degradation. The invention also relates to an oligonucleotide delivery
 CC complex comprising an oligonucleotide of the invention and a targeting
 CC agent, and a pharmaceutical composition comprising the oligonucleotide
 CC delivery complex. The oligonucleotides are able to induce either a cell-
 CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
 CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g., macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergenic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic
 CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antisense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention
 XX SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGCCTCGATGCGAGGGG 18
 Db 3 TGCCTCGATGCGAGGGG 20
 RESULT 2
 AAC80661
 ID AAC80661 standard; DNA; 20 BP.
 AC AAC80661;
 XX
 DT 14-FEB-2001 (first entry)
 XX
 DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:81.
 XX
 KW CpG oligodeoxynucleotide; unmethylated, antigen-presenting cell;
 KW immunogenic; cytokine release; natural killer cell; NK cell activation;
 KW cell-mediated immune response; T-cell response; humoral response;
 KW B-cell response; antibody production; immune response induction; vaccine;
 KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
 KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
 KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
 KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
 KW antimicrobial; antiallergic; protozoal; tubercular; dermatologic;
 KW antidiabetic; dermatologic; phosphorothioate; ss.
 OS Synthetic.
 XX
 XX WO2000061151-A2.
 PN
 XX

PD 19-OCT-2000.
 XX 12-APR-2000; 2000WO-US009839.
 PF
 XX 12-APR-1999; 99US-0128899P.
 PR
 XX (KLIN/) KLINMAN D.
 PA (ISHI/) ISHII K.
 PA (VERT/) VERTHELYI D.
 XX
 PI Klinman D, Ishii K, Verthelyi D;
 XX WPI; 2001-005880/01.
 DR
 XX Novel oligonucleotides useful for the prevention and treatment of
 PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
 PT resulting from exposure to a bio-warfare agent.
 PS Claim 4; Page 36; 46pp; English.
 CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
 CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
 CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
 CC optionally have phosphorothioate linkages which make them more resistant
 CC to degradation. The invention also relates to an oligonucleotide delivery
 CC complex comprising an oligonucleotide of the invention and a targeting
 CC agent, and a pharmaceutical composition comprising the oligonucleotide
 CC delivery complex. The oligonucleotides are able to induce either a cell-
 CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
 CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g., macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergenic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic
 CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antisense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention
 XX SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGCCTCGATGCGAGGGG 18
 Db 3 TGCCTCGATGCGAGGGG 20
 RESULT 3
 AAC80620
 ID AAC80620 standard; DNA; 20 BP.
 XX

AAC80620;
14-FEB-2001 (first entry)
Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:40.
CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
immunogenic; cytokine release; natural killer cell; NK cell activation;
cell-mediated immune response; T-cell response; humoral response; vaccine;
B-cell response; antibody production; immune response induction; allergic
allergy; asthma; infection; bacterial; viral; fungal; protozoal;
parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
immune deficiency; biological warfare agent; cytostatic; antiarthritic;
antimicrobial; anti-allergic; protozoacide; tuberculostatic;
antiasthmatic; dermatological; phosphorothioate; ss.
Synthetic.
WO200061151-A2.
19-OCT-2000.
12-APR-2000; 2000WO-US009839.
12-APR-1999; 99US-0128898P.
(KLIN/) KLINMAN D.
(ISHI/) ISHII K.
(VERT/) VERTHELYI D.
Klinman D, Ishii K, Verthelyi D;
WPI; 2001-006880/01.
Novel oligonucleotides useful for the prevention and treatment of
allergies, cancer, and autoimmune disorders and for ameliorating symptoms
resulting from exposure to a bio-warfare agent.
Claim 4; Page 30; 46pp; English.
The invention relates to novel immunogenic CpG oligodeoxynucleotides
(AAC80591-C80723). The oligonucleotide are at least 10 bases long and
comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
-3'. The central CpG motif is unmethylated, and the oligonucleotides
optionally have phosphorothioate linkages which make them more resistant
to degradation. The invention also relates to an oligonucleotide delivery
complex comprising an oligonucleotide of the invention and a targeting
agent, and a pharmaceutical composition comprising the oligonucleotide
delivery complex. The oligonucleotides are able to induce either a cell-
mediated (T-cell) response or a humoral (B-cell, antibody) response, with
oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
being able to induce a humoral response. It is thought that after
administration, the oligonucleotide acts on antigen-presenting cells
(e.g., macrophages and dendritic cells), which then release cytokines,
leading to activation of natural killer (NK) cells. A cell-mediated or
humoral response can then occur by activation of T- or B-cells. The
induction of an immune response is useful for treating, preventing or
ameliorating an allergic reaction (preferably asthma), or an infection,
where an immunogenic CpG oligonucleotide is administered either alone or
in combination with an anti-allergenic agent or anti-infectious agent.
The allergic conditions which may be treated include eczema, allergic
rhinitis, hayfever, urticaria, food allergies and other atopic
conditions, and the infections which may be treated include viral,
bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
leishmania and schistosomiasis. Immune response induction may also be
used in the treatment of an autoimmune disorder (e.g., lupus
erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
associated with immune system deficiency, and symptoms resulting from
exposure to an agent of biological warfare. An immunogenic CpG
oligonucleotide, either alone or in combination with an anti-cancer
agent, is useful for treating solid tumour cancer. The induction of an

CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGCCTCGATGCAGGGGGG 18
|||||
Db 3 TGCCTCGATGCAGGGGGG 20
RESULT 4
AAS09631
ID AAS09631 standard; DNA; 20 BP.
XX
AC AAS09631;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #81.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 40; 46pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or

CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematous and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria
 CC
 SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TGGCTCGATGCGAGGGGG 18
 Db 3 TGGCTCGATGCGAGGGGG 20
 RESULT 5
 AAS09590
 ID AAS09590 standard; DNA; 20 BP.
 AC AAS09590;
 XX
 XX 26-SEP-2001 (first entry)
 DT
 DE Immunoreactive CpG sequence-containing oligonucleotide #40.
 KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematous; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.
 XX Synthetic.
 OS
 XX WO200151500-A1.
 PN
 XX 19-JUL-2001.
 PD
 XX 12-JAN-2001; 2001WO-US001122.
 PF
 XX 14-JAN-2000; 2000US-0176115P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Kliman D, Ishii K, Verthelyi D;
 PI
 XX WPI; 2001-442129/47.
 DR
 XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.
 XX
 PS Claim 5; Page 33; 48pp; English.
 FS
 XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,

CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematous and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria
 CC
 SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TGGCTCGATGCGAGGGGG 18
 Db 3 TGGCTCGATGCGAGGGGG 20
 RESULT 6
 AAS09632
 ID AAS09632 standard; DNA; 20 BP.
 AC AAS09632;
 XX
 XX 26-SEP-2001 (first entry)
 DT
 DE Immunoreactive CpG sequence-containing oligonucleotide #82.
 KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematous; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.
 XX Synthetic.
 OS
 XX WO200151500-A1.
 PN
 XX 19-JUL-2001.
 PD
 XX 12-JAN-2001; 2001WO-US001122.
 PF
 XX 14-JAN-2000; 2000US-0176115P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Kliman D, Ishii K, Verthelyi D;
 PI
 XX WPI; 2001-442129/47.
 DR
 XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.
 XX
 PS Claim 5; Page 40; 48pp; English.
 FS
 XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,

CC ODN are useful for inducing an immune response, preferably a cell-mediated immune response, involving non-B cell activation, interferon gamma (IFN-gamma) production or a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma, cancer, e.g. solid tumor cancer, a disease associated with the immune system e.g. autoimmune disorder or an immune system deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antisense therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines against hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, anthrax and Listeria

XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGGTCGATGCAGGGGG 18
|||||
Db 3 TCGGTCGATGCAGGGGG 20

RESULT 7
ABK46510
ID ABK46510 standard; DNA; 20 BP.
AC ABK46510;
XX
XX
DT 05-JUN-2002 (first entry)
XX
DE Immunostimulatory unmethylated CpG oligodeoxynucleotide #100.
XX
XX unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine;
KW Paramyxoviridae; F protein; respiratory syncytial virus; RSV;
KW viral bronchiolitis; pneumonia; infectious pulmonary disease;
KW bronchopulmonary dysplasia; congenital heart condition; ss.
XX
OS Synthetic.

XX
XX WO200211761-A2.
XX
XX 14-FEB-2002.
XX
XX 09-AUG-2001; 2001WO-US041633.
XX
XX 10-AUG-2000; 2000US-0224011P.
XX
XX 01-SEP-2000; 2000US-0229307P.
XX
XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
PA
XX Mond JJ, Prince G, Klinman DM;
XX
XX WPI; 2002-227118/28.
XX

XX Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of Paramyxoviridae F protein, and one or more CpG (cytosine followed by guanine linked by phosphate bond)-oligodeoxynucleotides.

XX Claim 4; Page 9; 30pp; English.

XX The invention describes a vaccine comprising one or more epitopes of a Paramyxoviridae F protein, and one or more CpG (cytosine followed by guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The

CC vaccine is useful for vaccinating a patient especially against viruses of the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the primary cause of viral bronchiolitis and pneumonia in infants and children, and infectious pulmonary disease in infants. RSV has been particularly implicated in death of infants that are premature, have bronchopulmonary dysplasia, or congenital heart conditions. This sequence represents an oligodeoxynucleotide that can be used in the creation of the vaccine

XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGGTCGATGCAGGGGG 18
|||||
Db 3 TCGGTCGATGCAGGGGG 20

RESULT 8
ABK46468
ID ABK46468 standard; DNA; 20 BP.
XX
AC ABK46468;
XX
DT 05-JUN-2002 (first entry)
XX
DE Immunostimulatory unmethylated CpG oligodeoxynucleotide #58.
XX
XX unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine;
KW Paramyxoviridae; F protein; respiratory syncytial virus; RSV;
KW viral bronchiolitis; pneumonia; infectious pulmonary disease;
KW bronchopulmonary dysplasia; congenital heart condition; ss.
XX
OS Synthetic.

XX WO200211761-A2.

XX 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US041633.

XX 10-AUG-2000; 2000US-0224011P.

XX 01-SEP-2000; 2000US-0229307P.

XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

XX Mond JJ, Prince G, Klinman DM;

XX WPI; 2002-227118/28.

XX Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of Paramyxoviridae F protein, and cytosine followed by guanine linked by phosphate bond-oligodeoxynucleotides.

XX Claim 4; Page 8; 30pp; English.

XX The invention describes a vaccine comprising one or more epitopes of a Paramyxoviridae F protein, and one or more CpG (cytosine followed by guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The vaccine is useful for vaccinating a patient especially against viruses of the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the primary cause of viral bronchiolitis and pneumonia in infants and children, and infectious pulmonary disease in infants. RSV has been particularly implicated in death of infants that are premature, have bronchopulmonary dysplasia, or congenital heart conditions. This sequence represents an oligodeoxynucleotide that can be used in the creation of the vaccine

XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTCGATCGAGGGGG 18
| | | | | | | | | | | | | | | | | |
Db 3 TCGTCGATCGAGGGGG 20

RESULT 9
ABK46509
ID ABK46509 standard; DNA; 20 BP.
AC ABK46509;
XX
DT 05-JUN-2002 (first entry)
XX
DE Immunostimulatory unmethylated CpG oligodeoxynucleotide #99.
XX
KW unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine;
KW Paramyxoviridae; F protein; respiratory syncytial virus; RSV;
KW viral bronchiolitis; pneumonia; infectious pulmonary disease;
KW bronchopulmonary dysplasia; congenital heart condition; ss.
XX
OS Synthetic.
XX
PN WO200211761-A2.
XX
DT 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US041633.
XX
PR 10-AUG-2000; 2000US-0224011P.
XX
PA 01-SEP-2000; 2000US-0229307P.
XX
PI (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
PN Mond JJ, Prince G, Klinman DM;
XX
DR WPI; 2002-2271138/28.
XX
PT Vaccine for immunizing patient against respiratory syncytial virus, has
PT epitopes of Paramyxoviridae F protein, and cytosine followed by guanine
PT linked by phosphate bond-oligodeoxynucleotides.
XX
PS Claim 4; Page 9; 30pp; English.
XX
CC The invention describes a vaccine comprising one or more epitopes of a
CC Paramyxoviridae F protein, and one or more CpG (cytosine followed by
CC guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The
CC vaccine is useful for vaccinating a patient especially against viruses of
CC the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the
CC primary cause of viral bronchiolitis and pneumonia in infants and
CC children, and infectious pulmonary disease in infants. RSV has been
CC particularly implicated in death of infants that are premature, have
CC bronchopulmonary dysplasia, or congenital heart conditions. This sequence
CC represents an oligodeoxynucleotide that can be used in the creation of
CC the vaccine
XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTCGATCGAGGGGG 18
| | | | | | | | | | | | | | | | | |
Db 3 TCGTCGATCGAGGGGG 20

RESULT 10
ACC48298
ID ACC48298 standard; DNA; 20 BP.
XX

AC ACC48298;
XX
DT 11-AUG-2003 (first entry)
XX
DE CpG oligodeoxynucleotide DV35 used for dendritic cell maturation.
XX
KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
KW cytostatic; immunostimulant; gene therapy; ss.
XX
OS Synthetic.
XX
PN WO2003020884-A2.
XX
PD 13-MAR-2003.
XX
PF 13-AUG-2002; 2002WO-US025732.
XX
PR 14-AUG-2001; 2001US-0312190P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Gursel M, Verthelyi D;
XX
DR WPI; 2003-300874/29.
XX
PT Generating mature dendritic cells for tumor immunotherapy or as vaccines
PT for activating the immune system to treat diseases such as cancer,
PT comprises contacting a dendritic cell precursor with a D type
PT oligodeoxynucleotide.
XX
PS Disclosure; Fig 8; 69pp; English.
XX
CC The present sequence is that of D type CpG oligodeoxynucleotide DV28, an
CC example of claimed D type oligodeoxynucleotides (see ACC48298) of the
CC invention. Mature dendritic cells are obtained by contacting a dendritic
CC cell precursor, such as a monocyte, with such an oligodeoxynucleotide.
CC The method is useful for generating mature dendritic cells and enhancing
CC T cell responses, thus enhancing antigen presentation. Mature dendritic
CC cells are useful for tumour immunotherapy, for augmenting an immune
CC response to an infectious agent or to a vaccine, and as vaccines to
CC prevent future infection or to activate the immune system to treat
CC diseases such as cancer. Mature dendritic cells may also be used to
CC produce activated T lymphocytes
XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTCGATCGAGGGGG 18
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Db 3 TCGTCGATCGAGGGGG 20

RESULT 11
ACC48312
ID ACC48312 standard; DNA; 20 BP.
XX
AC ACC48312;
XX
DT 11-AUG-2003 (first entry)
XX
DE CpG oligodeoxynucleotide DV52.
XX
KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
KW cytostatic; immunostimulant; gene therapy; ss.
XX
OS Synthetic.
XX
PN WO2003020884-A2.
XX
PD 13-MAR-2003.

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XX
PF 13-AUG-2002; 2002WO-US025732.
XX
XX 14-AUG-2001; 2001US-0312190P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Klinman DM, Gursel M, Verthelyi D;
XX
XX WPI; 2003-300874/29.
XX
XX Generating mature dendritic cells for tumor immunotherapy or as vaccines
XX for activating the immune system to treat diseases such as cancer,
XX comprises contacting a dendritic cell precursor with a D type
XX oligodeoxynucleotide.
XX
XX Disclosure; Fig 8; 69pp; English.
XX
XX The present sequence is that of CpG oligodeoxynucleotide DV52 of the
XX invention. A claimed method for generating dendritic cells involves
XX contacting a dendritic cell precursor, especially a monocyte, with a D
XX type oligodeoxynucleotide (see ACC48294) containing a central
XX unmethylated CpG motif. The method is useful for generating mature
XX dendritic cells and enhancing T cell responses, thus enhancing antigen
XX presentation. Mature dendritic cells are useful for tumour immunotherapy,
XX for augmenting an immune response to an infectious agent or to a vaccine,
XX and as vaccines to prevent future infection or to activate the immune
XX system to treat diseases such as cancer. Mature dendritic cells may also
XX be used to produce activated T lymphocytes
XX
XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 7; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 17;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TGGCTCGATCGAGGGGG 18
XX |||||
XX 3 TGGCTCGATCGAGGGGG 20
XX
XX Db
XX
XX RESULT 12
XX ACC48306
XX ID ACC48306 standard; DNA; 20 BP.
XX
XX ACC48306;
XX
XX 11-AUG-2003 (first entry)
XX
XX CpG oligodeoxynucleotide used for dendritic cell maturation.
XX
XX CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
XX cytostatic; immunostimulant; gene therapy; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_difference 1 /*tag= a
XX FT /*note= "N is any base (especially G) or no base"
XX misc_difference 2 /*tag= b
XX FT /*note= "N is any base (especially G) or no base"
XX
XX WO2003020884-A2.
XX
XX 13-MAR-2003.
XX
XX 13-AUG-2002; 2002WO-US025732.
XX
XX 14-AUG-2001; 2001US-0312190P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX

```

XX Klimman DM, Gursel M, Verthelyi D;
XX WPI; 2003-300874/29.
XX
XX Generating mature dendritic cells for tumor immunotherapy or as vaccines
XX for activating the immune system to treat diseases such as cancer,
XX PT comprises contacting a dendritic cell precursor with a D type
XX oligodeoxynucleotide.
XX
XX Disclosure; Page 26; 69pp; English.
XX
XX The present sequence is that of a D type CpG oligodeoxynucleotide that is
XX an example of claimed D type oligodeoxynucleotides (see ACC48294) of the
XX invention. Mature dendritic cells are obtained by contacting a dendritic
XX cell precursor, such as a monocyte, with such an oligodeoxynucleotide.
XX The method is useful for generating mature dendritic cells and enhancing
XX T cell responses, thus enhancing antigen presentation. Mature dendritic
XX cells are useful for tumor immunotherapy, for augmenting an immune
XX response to an infectious agent or to a vaccine, and as vaccines to
XX prevent future infection or to activate the immune system to treat
XX diseases such as cancer. Mature dendritic cells may also be used to
XX CC produce activated T lymphocytes
XX
XX Sequence 20 BP; 2 A; 3 C; 10 G; 3 T; 0 U; 2 Other;
XX

Query Match 100.0%; Score 18; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. NO. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

QY 1 TGGTCGATGCAGGGGGG 18
Db 3 TGGTCGATGCAGGGGGG 20
XXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXX

RESULT 13
ACC48319
ID ACC48319 standard; DNA; 20 BP.
AC AC ACC48319;
XX
XX 11-AUG-2003 (first entry)
XX
XX CpG oligodeoxynucleotide DV28.
XX
XX CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
XX cytostatic; immunostimulant; gene therapy; ss.
XX Synthetic.
XX OS
XX WO2003020884-A2.
XX PN
XX 13-MAR-2003.
XX PD
XX 13-AUG-2002; 2002WO-US025732.
XX PP
XX 14-AUG-2001; 2001US-0312190P.
XX PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Klimman DM, Gursel M, Verthelyi D;
XX WPI; 2003-300874/29.
XX
XX Generating mature dendritic cells for tumor immunotherapy or as vaccines
XX for activating the immune system to treat diseases such as cancer,
XX PT comprises contacting a dendritic cell precursor with a D type
XX oligodeoxynucleotide.
XX
XX Disclosure; Fig 8; 69pp; English.
XX
XX The present sequence is that of CpG oligodeoxynucleotide DV28 of the
XX invention. A claimed method for generating dendritic cells involves
XX CC
XX

CC contacting a dendritic cell precursor, especially a monocyte, with a D
CC type oligodeoxynucleotide (see ACC48294) containing a central
CC unmethylated CpG motif. The method is useful for generating mature
CC dendritic cells and enhancing T cell responses, thus enhancing antigen
CC presentation. Mature dendritic cells are useful for tumour immunotherapy.
CC for augmenting an immune response to an infectious agent or to a vaccine,
CC and as vaccines to prevent future infection or to activate the immune
CC system to treat diseases such as cancer. Mature dendritic cells may also
CC be used to produce activated T lymphocytes

XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGTCGATGCAGGGGG 18
|||
Db 3 TGGTCGATGCAGGGGG 20

RESULT 14
ACC83117
ID ACC83117 standard; DNA; 20 BP.
XX
AC ACC83117;
XX
DT 27-AUG-2003 (first entry)
XX
DE D class CpG ODN sequence useful for encapsulating in SSCL, DV28.

XX Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
KW tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
KW thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
KW schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
KW asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
KW CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
KW multiple sclerosis; infection; tumour; ss.

XX Unidentified.
OS
XX WO2003040308-A2.
XX
PN 15-MAY-2003.
XX
PD 29-JUL-2002; 2002WO-US024235.
XX
PF 27-JUL-2001; 2001US-0308283P.
XX
PR 25-JUL-2002; 2002US-00206407.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Klinman DM, Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK;
XX WPI; 2003-482260/45.

XX Cationic liposome composition for delivering oligodeoxynucleotides
PT including a CpG motif in clinical applications, comprises a cationic
PT lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
XX
XX Disclosure; Fig 10C; 110pp; English.

XX The invention relates to sterically stabilised cationic liposomes (SSCL)
CC which comprises a cationic lipid, a co-lipid, stabilising agent and
CC encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.
CC The invention is useful in pharmaceutical composition for impairing
CC growth of a solid tumour cell (e.g. human tumour cell) bearing an
CC interleukin-13 receptor in a subject; for stimulating an immune response,
CC which is expression of a cytokine (e.g. interferon gamma), particularly
CC immunotherapeutic response against tumours or stimulating an in vivo or
CC an in vitro immune cell, and for inducing an immune response against an
CC infectious agent e.g. virus, bacteria and fungus. It is also useful for
CC delivering oligodeoxynucleotides including a CpG motif in clinical

CC applications; for treating infectious diseases (e.g. tularemia, malaria,
CC francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
CC (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer
CC etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,
CC bronchial or allergic asthma, urticaria, food allergies), autoimmune
CC diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and
CC multiple sclerosis) and psoriasis. The present sequence is a D class CpG
CC ODN potentially useful for encapsulating in SSCL

XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGTCGATGCAGGGGG 18
|||
Db 3 TGGTCGATGCAGGGGG 20

RESULT 15
ACC83124
ID ACC83124 standard; DNA; 20 BP.
XX
AC ACC83124;
XX
DT 27-AUG-2003 (first entry)
XX
DE D class CpG ODN sequence useful for encapsulating in SSCL, DV52.

XX Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
KW tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
KW thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
KW schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
KW asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
KW CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
KW multiple sclerosis; infection; tumour; ss.

XX Unidentified.
OS
XX WO2003040308-A2.
XX
PN 15-MAY-2003.
XX
PD 29-JUL-2002; 2002WO-US024235.
XX
PF 27-JUL-2001; 2001US-0308283P.
XX
PR 25-JUL-2002; 2002US-00206407.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Klinman DM, Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK;
XX WPI; 2003-482260/45.

XX Cationic liposome composition for delivering oligodeoxynucleotides
PT including a CpG motif in clinical applications, comprises a cationic
PT lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
XX
XX Disclosure; Fig 10C; 110pp; English.

XX The invention relates to sterically stabilised cationic liposomes (SSCL)
CC which comprises a cationic lipid, a co-lipid, stabilising agent and
CC encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.
CC The invention is useful in pharmaceutical composition for impairing
CC growth of a solid tumour cell (e.g. human tumour cell) bearing an
CC interleukin-13 receptor in a subject; for stimulating an immune response,
CC which is expression of a cytokine (e.g. interferon gamma), particularly
CC immunotherapeutic response against tumours or stimulating an in vivo or
CC an in vitro immune cell, and for inducing an immune response against an
CC infectious agent e.g. virus, bacteria and fungus. It is also useful for
CC delivering oligodeoxynucleotides including a CpG motif in clinical
CC applications; for treating infectious diseases (e.g. tularemia, malaria,

CC francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
 CC (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer
 CC etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,
 CC bronchial or allergic asthma, urticaria, food allergies), autoimmune
 CC diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and
 CC multiple sclerosis) and psoriasis. The present sequence is a D class CpG
 CC ODN potentially useful for encapsulating in SSCL

XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGCTCGATCGAGGGGG 18
 |||||
 Db 3 TGGCTCGATCGAGGGGG 20

Search completed: July 2, 2004, 08:31:35
 Job time : 134.89 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:09:30 ; Search time 28.2073 Seconds
(without alignments)
354.132 Million cell updates/sec

Title: US-10-068-160-16

Perfect score: 18

Sequence: 1 tgcgtcgatgcagggggg 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:**
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4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.4	80.0	2870	4	US-09-799-875-16
2	14.4	80.0	2891	4	US-09-578-441-1
3	14.4	80.0	4403765	3	US-09-103-840A-2
4	14.4	80.0	4411529	3	US-09-103-840A-1
5	14	77.8	759	4	US-09-252-991A-1486
6	14	77.8	1308	4	US-09-252-991A-1592
7	14	77.8	1356	4	US-09-252-991A-1425
8	14	77.8	3591	4	US-09-252-991A-1690
9	13.8	76.7	20	4	US-09-659-845A-106
10	13.8	76.7	552	4	US-09-252-991A-6091
11	13.8	76.7	585	4	US-09-252-991A-6007
12	13.8	76.7	594	4	US-09-489-039A-7023
13	13.8	76.7	609	4	US-09-252-991A-6173
14	13.8	76.7	642	4	US-09-252-991A-6014
15	13.8	76.7	655	3	US-08-861-774B-55
16	13.8	76.7	822	4	US-09-252-991A-6377
17	13.8	76.7	885	4	US-09-252-991A-7552
18	13.8	76.7	906	4	US-09-489-039A-3080
19	13.8	76.7	912	4	US-09-252-991A-7811
20	13.8	76.7	978	4	US-09-252-991A-6384
21	13.8	76.7	1242	4	US-09-252-991A-7949
22	13.8	76.7	1255	4	US-09-659-845A-104
23	13.8	76.7	1365	4	US-09-659-845A-10
24	13.8	76.7	1392	4	US-09-489-039A-4664
25	13.8	76.7	1571	1	US-08-726-525-1
26	13.8	76.7	1571	1	US-08-487-942-1
27	13.8	76.7	1571	2	US-08-726-036A-1

ALIGNMENTS

RESULT 1

US-09-799-875-16

; Sequence 16, Application US/09799875

; Patent No. 6638721

; GENERAL INFORMATION:

; APPLICANT: Meyers, Rachel

; APPLICANT: Kapeller-Libermann, Rosana

; APPLICANT: Williamson, Mark

; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses

; FILE OF INVENTION: Therefor

; FILE REFERENCE: 35800/209596

; CURRENT APPLICATION NUMBER: US/09/799,875

; CURRENT FILING DATE: 2001-03-06

; PRIOR APPLICATION NUMBER: 60/182,059

; PRIOR FILING DATE: 2000-02-11

; PRIOR APPLICATION NUMBER: 09/659,287

; PRIOR FILING DATE: 2000-09-12

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 16

; LENGTH: 2870

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (114)...(2000)

; US-09-799-875-16

Query Match 80.0%; Score 14.4; DB 4; Length 2870;

Best Local Similarity 93.8%; Pred. No. 2.1e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGTCGATGCAGGGGG 18

Db 109 CGCGATGCAGGGGG 124

RESULT 2

US-09-578-441-1

; Sequence 1, Application US/09578441

; Patent No. 6562571

; GENERAL INFORMATION:

; APPLICANT: Wu, J.H. David

; APPLICANT: Omata, Takeshi

; APPLICANT: Mantalaris, Athanasios

; APPLICANT: Chen, Yi-Guang

; APPLICANT: Tsai, Ying-Chueh

; TITLE OF INVENTION: HUMAN HEME-REGULATED INITIATION FACTOR 2.ALPHA KINASE

; FILE REFERENCE: 176/60571

; CURRENT APPLICATION NUMBER: US/09/578,441

Sequence 1, Appli
Sequence 7681, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 66, Appli
Sequence 66, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 105, Appli
Sequence 3, Appli
Patent No. 546595
Sequence 5, Appli
Patent No. 546585
Sequence 2941, Ap
Sequence 8040, Ap

28 13.8 76.7 1571 4 US-09-083-516-1
c 29 13.8 76.7 1794 4 US-09-252-991A-7681
c 30 13.8 76.7 5561 2 US-08-400-159-1
c 31 13.8 76.7 5561 3 US-08-611-729A-1
c 32 13.8 76.7 6814 4 US-09-484-970B-66
c 33 13.8 76.7 6814 4 US-09-484-970B-66
c 34 13.8 76.7 8378 5 PCT-US91-09055-1
c 35 13.8 76.7 32155 4 US-08-311-731A-1
c 36 13.8 76.7 536165 4 US-09-214-808-1
c 37 13.8 76.7 4403765 3 US-09-103-840A-2
c 38 13.8 76.7 4411529 3 US-09-103-840A-1
c 39 13.4 74.4 20 4 US-09-659-845A-105
c 40 13.4 74.4 171 4 US-09-187-108-3
c 41 13.4 74.4 171 6 546595-4
c 42 13.4 74.4 253 4 US-09-187-108-5
c 43 13.4 74.4 253 6 546595-5
c 44 13.4 74.4 333 4 US-09-489-039A-2941
c 45 13.4 74.4 471 4 US-09-252-991A-8040

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; CURRENT FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 50/135,713
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2891
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-578-441-1

Query Match      80.0%; Score 14.4; DB 4; Length 2891;
Best Local Similarity 93.8%; Pred.No.2.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGTCGATCCAGGGGG 18
    |||||
DB 77 CGCGATCCAGGGGG 92

RESULT 3
US-09-103-840A-2
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match      80.0%; Score 14.4; DB 3; Length 4403765;
Best Local Similarity 93.8%; Pred.No.1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGTCGATCCAGGGGG 18
    |||||
DB 822321 CGTCGATCCAGGGGG 822336

RESULT 4
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529

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Db 369 TGGTCGATGCAGG 362

RESULT 7

US-09-252-991A-1425/c
; Sequence 1425, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1425
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1425

Query Match 77.8%; Score 14; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGTCGATGCAGG 14
||| ||||| |||||
Db 979 TGGTCGATGCAGG 966

RESULT 8

US-09-252-991A-1690
; Sequence 1690, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1690
; LENGTH: 3591
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1690

Query Match 77.8%; Score 14; DB 4; Length 3591;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGTCGATGCAGG 14
||| ||||| |||||
Db 295 TGGTCGATGCAGG 308

RESULT 9

US-09-659-845A-106/c
; Sequence 106, Application US/09659845A
; Patent No. 6492170
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 9 EXPRESSION

; FILE REFERENCE: RTS-0183
; CURRENT APPLICATION NUMBER: US/09/659,845A
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 106
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-845A-106

Query Match 76.7%; Score 13.8; DB 4; Length 20;
Best Local Similarity 88.2%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCGTCGATGCAGGGGG 17
||| ||||| |||||
Db 18 TCGCGCATGCAGGGTG 2

RESULT 10

US-09-252-991A-6091/c
; Sequence 6091, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6091
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6091

Query Match 76.7%; Score 13.8; DB 4; Length 552;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCGTCGATGCAGGGGG 18
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Db 123 GCGTTCGTCAGGGGG 107

RESULT 11

US-09-252-991A-6007/c
; Sequence 6007, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6007
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6007

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Query Match      76.7%; Score 13.8; DB 4; Length 585;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCGTCGATCGAGGGGG 18
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Db      354 GCGTCGATCGAGGGGG 338

RESULT 12
US-09-489-039A-7023/c
; Sequence 7023, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7023
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7023

Query Match      76.7%; Score 13.8; DB 4; Length 594;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TCGGTCGATCGAGGGGG 17
      |||||
Db      262 TCGGCGAGCAGGGGG 246

RESULT 13
US-09-252-991A-6173/c
; Sequence 6173, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6173
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6173

Query Match      76.7%; Score 13.8; DB 4; Length 609;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCGTCGATCGAGGGGG 18
      |||||
Db      83 GCGTTGCTGCAGGGGG 67

RESULT 14
US-09-252-991A-6014/c
; Sequence 6014, Application US/09252991A
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; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6014
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6014

Query Match      76.7%; Score 13.8; DB 4; Length 642;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCGTCGATCGAGGGGG 18
      |||||
Db      229 GCGTTGCTGCAGGGGG 213

RESULT 15
US-08-861-774E-55
; Sequence 55, Application US/08861774E
; Patent No. 6297007
; GENERAL INFORMATION:
; APPLICANT: Waters, Barbara
; APPLICANT: Miao, Vivian
; APPLICANT: Ho, Yap
; APPLICANT: Tong, Seow
; TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
; TITLE OF INVENTION: BIOACTIVE MOLECULES
; FILE REFERENCE: 9993-006
; CURRENT APPLICATION NUMBER: US/08/861,774E
; CURRENT FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Peltigera neopolydactyla
US-08-861-774E-55

Query Match      76.7%; Score 13.8; DB 3; Length 655;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCGTCGATCGAGGGGG 18
      |||||
Db      75 GCGTTATCGAGGGGG 91

Search completed: July 2, 2004, 13:37:40
Job time : 44.2073 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:11:05 ; Search time 138.732 Seconds
(without alignments)
625.926 Million cell updates/sec

Title: US-10-068-160-16

Perfect score: 18

Sequence: 1 tgcgtcgatgcagg9999 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*

14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	15	US-10-068-160-16
2	18	100.0	20	15	US-10-068-160-7
3	18	100.0	20	15	US-10-194-035-40
4	18	100.0	20	15	US-10-194-035-81
5	18	100.0	20	15	US-10-194-035-82
6	18	100.0	20	17	US-10-666-022-4
7	18	100.0	20	17	US-10-666-022-16
8	17	94.4	19	15	US-10-194-035-83
9	16.4	91.1	18	13	US-09-874-991C-503
10	16.4	91.1	18	13	US-09-874-991C-513
11	16.4	91.1	18	13	US-09-874-991C-551
12	16.4	91.1	18	15	US-10-068-160-12
13	16.4	91.1	18	15	US-10-068-160-14
14	16.4	91.1	18	15	US-10-068-160-18

15	16.4	91.1	18	15	US-10-068-160-20
16	16.4	91.1	20	13	US-09-874-991C-494
17	16.4	91.1	20	13	US-09-874-991C-497
18	16.4	91.1	20	13	US-09-874-991C-502
19	16.4	91.1	20	13	US-09-874-991C-505
20	16.4	91.1	20	13	US-09-874-991C-508
21	16.4	91.1	20	13	US-09-874-991C-512
22	16.4	91.1	20	13	US-09-874-991C-538
23	16.4	91.1	20	13	US-09-874-991C-541
24	16.4	91.1	20	13	US-09-874-991C-546
25	16.4	91.1	20	13	US-09-874-991C-550
26	16.4	91.1	20	15	US-10-068-160-1
27	16.4	91.1	20	15	US-10-068-160-26
28	16.4	91.1	20	15	US-10-068-160-31
29	16.4	91.1	20	15	US-10-068-160-38
30	16.4	91.1	20	15	US-10-068-160-54
31	16.4	91.1	20	15	US-10-194-035-32
32	16.4	91.1	20	15	US-10-194-035-34
33	16.4	91.1	20	15	US-10-194-035-37
34	16.4	91.1	20	15	US-10-194-035-38
35	16.4	91.1	20	15	US-10-194-035-39
36	16.4	91.1	20	15	US-10-194-035-41
37	16.4	91.1	20	15	US-10-194-035-43
38	16.4	91.1	20	15	US-10-194-035-72
39	16.4	91.1	20	15	US-10-194-035-102
40	16.4	91.1	20	17	US-10-666-022-1
41	16.4	91.1	20	17	US-10-666-022-3
42	16.4	91.1	20	17	US-10-666-022-6
43	16.4	91.1	20	17	US-10-666-022-8
44	16.4	91.1	20	17	US-10-666-022-176
45	16.4	91.1	20	17	US-10-666-022-177

ALIGNMENTS

RESULT 1

US-10-068-160-16
; Sequence 16, Application US/10068160
; Publication No. US2003006040A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODENDROCYTE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-16

Query Match 100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTCGATGCAGGGGG 18
DB 1 TCGTCGATGCAGGGGG 18

RESULT 2

US-10-068-160-7

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; Sequence 7, Application US/10068160
; Publication No. US2003006040A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1998-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-7

Query Match      100.0%; Score 18; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGGTGCGATGCAGGGGGG 18
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DB 3 TGGGTGCGATGCAGGGGGG 20

RESULT 3
US-10-194-035-40
; Sequence 40, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-40

Query Match      100.0%; Score 18; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGGTGCGATGCAGGGGGG 18
   |||||
DB 3 TGGGTGCGATGCAGGGGGG 20

RESULT 4
US-10-194-035-81
; Sequence 81, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-81

Query Match      100.0%; Score 18; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGGTGCGATGCAGGGGGG 18
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DB 3 TGGGTGCGATGCAGGGGGG 20

RESULT 5
US-10-194-035-82
; Sequence 82, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-82

Query Match      100.0%; Score 18; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGGTGCGATGCAGGGGGG 18
   |||||
DB 3 TGGGTGCGATGCAGGGGGG 20

RESULT 6
US-10-666-022-4
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Sequence 4, Application US/10666022
 Publication No. US20040105872A1
 GENERAL INFORMATION:
 APPLICANT: The Government of the United States of America, as represented by the
 APPLICANT: Secretary of the Department of Health and Human Services
 APPLICANT: Klinman, Dennis M.
 APPLICANT: Verthelyi, Daniela
 TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
 SUBJECTS WITH IMMUNOSTIMULATORY CPG
 FILE REFERENCE: 4239-66899
 CURRENT APPLICATION NUMBER: US/10/666,022
 CURRENT FILING DATE: 2003-09-17
 PRIOR APPLICATION NUMBER: US 60/411,944
 PRIOR FILING DATE: 2002-09-18
 NUMBER OF SEQ ID NOS: 181
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 4
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: synthetic
 NAME/KEY: misc_feature
 LOCATION: (1)..(20)
 OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
 US-10-666-022-4

Query Match 100.0%; Score 18; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGTCGATCGAGGGGG 18
 |||||
 DB 3 TGGTCGATCGAGGGGG 20

RESULT 7

US-10-666-022-16
 Sequence 16, Application US/10666022
 Publication No. US20040105872A1
 GENERAL INFORMATION:
 APPLICANT: The Government of the United States of America, as represented by the
 APPLICANT: Secretary of the Department of Health and Human Services
 APPLICANT: Klinman, Dennis M.
 APPLICANT: Verthelyi, Daniela
 TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
 SUBJECTS WITH IMMUNOSTIMULATORY CPG
 FILE REFERENCE: 4239-66899
 CURRENT APPLICATION NUMBER: US/10/666,022
 CURRENT FILING DATE: 2003-09-17
 PRIOR APPLICATION NUMBER: US 60/411,944
 PRIOR FILING DATE: 2002-09-18
 NUMBER OF SEQ ID NOS: 181
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 16
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: synthetic
 US-10-666-022-16

Query Match 100.0%; Score 18; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGTCGATCGAGGGGG 18
 |||||
 DB 3 TGGTCGATCGAGGGGG 20

RESULT 8

US-09-874-991C-513

Sequence 513, Application US/09874991C

Publication No. US20040052763A1

US-10-194-035-83
 Sequence 83, Application US/10194035
 Publication No. US20030144229A1
 GENERAL INFORMATION:
 APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
 APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
 APPLICANT: KLINMAN, Dennis
 APPLICANT: ISHII, Ken
 APPLICANT: VERTHELYI, Daniela
 TITLE OF INVENTION: OLIGODENOVIRUS AND ITS USE TO INDUCE AN IMMUNE RESPONSE
 FILE REFERENCE: 4239-63317
 CURRENT APPLICATION NUMBER: US/10/194,035
 CURRENT FILING DATE: 2002-07-12
 PRIOR APPLICATION NUMBER: PCT/US01/01122
 PRIOR FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: US 60/176,115
 PRIOR FILING DATE: 2000-01-14
 NUMBER OF SEQ ID NOS: 119
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 83
 LENGTH: 19
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
 US-10-194-035-83

Query Match 94.4%; Score 17; DB 15; Length 19;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGTCGATCGAGGGGG 17
 |||||
 DB 3 TGGTCGATCGAGGGGG 19

RESULT 9

US-09-874-991C-503
 Sequence 503, Application US/09874991C
 Publication No. US20040052763A1
 GENERAL INFORMATION:
 APPLICANT: MOND, JAMES J.
 APPLICANT: FLORA, MICHAEL
 APPLICANT: KLINMAN, DENNIS M.
 TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
 FILE REFERENCE: 07787.0042-0
 CURRENT APPLICATION NUMBER: US/09/874,991C
 CURRENT FILING DATE: 2001-06-07
 PRIOR APPLICATION NUMBER: 60/209,797
 PRIOR FILING DATE: 2000-06-07
 NUMBER OF SEQ ID NOS: 620
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 503
 LENGTH: 18
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
 US-09-874-991C-503

Query Match 91.1%; Score 16.4; DB 13; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGTCGATCGAGGGGG 18
 |||||
 DB 1 TGCATCGATCGAGGGGG 18

RESULT 10

US-09-874-991C-513
 Sequence 513, Application US/09874991C
 Publication No. US20040052763A1

Search completed: July 2, 2004, 13:58:25
Job time : 139.732 secs

Qy	2 GCACCGGCGCAGGGGG 18 943 GCGCCGCCGCAGGGGG 959
Dd	
RESULT 4 BUS40484/c	
LOCUS	BUS40484 linear EST 13-SEP-2002
DEFINITION	AGENCOURT_10325169 NIH_MGC_18 Homo sapiens CDNA clone IMAGE:6571942 5' mRNA sequence.
ACCESSION	BUS40484
VERSION	BUS40484.1 GI:22850925
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Theria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1417) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: DCTD/BTP/Gazdar CDNA Library Preparation: Rubin Laboratory DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) Agencourt Bioscience Corporation Cloned through the MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LMC2763 row: d column: 22 High quality sequence start: 57 High quality sequence stop: 392. Location/Qualifiers
FEATURES	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone=IMAGE:6571942 /tissue type="large cell carcinoma" /lab host="DH10B (phage-resistant)" /clone lib="NH1 MGC 18"
SOURCE	/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: This is a NIH_MGC library."
ORIGIN	
Query Match	94.4%; Score 17; DB 13; Length 1417;
Best Local Similarity	100.0%; Pred. No. 2.6e+04;
Matches	17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	2 GCGCGCGCGCAGGGGG 18
Dd	852 GCGCGCGCGCAGGGGG 836
RESULT 5 CNLS01T3H/c	
LOCUS	CNLS01T3H/c linear GSS 01-SEP-2000
DEFINITION	Tetraodon nigroviridis genome survey sequence T7 end of clone 194E11 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION	AL166022
VERSION	AL166022.1 GI:7803760
KEYWORDS	GSS: genome survey sequence.
SOURCE	Tetraodon nigroviridis
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Tetraodon.	REFERENCE AUTHORS
Ruest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,F., Quetier,P., Saurin,W. and Weissenbach,J. Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000) 20296633 10835645	TITLE JOURNAL MEDLINE PUBLISHED PUBMED REFERENCE AUTHORS
Ruest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,P., Saurin,W. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000) 20359837 10899143	TITLE JOURNAL MEDLINE PUBLISHED PUBMED REFERENCE AUTHORS
Direct Submission Submitted(12-APR-2000) GenomeScope - Centre National de Sequence : BP 191 91006 EVRY cedex - FRANCE [E-mail : seqref@genoscope.cns.fr] - Web : www.genoscope.cns.fr This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon .	COMMENT
Location/Qualifiers 1..630 /organism="Tetraodon nigroviridis" /mol_type="genomic DNA" /db_xref="taxon:99883" /clone="194E11" /clone_lib="G" /note="Genoscope sequence ID : COAG194AC06LP1-end ; T7"	FEATURES SOURCE
Query Match 92.2% ; Score 16.6; DB 29; Length 630; Best Local Similarity 94.1% ; Pred. NO. 3.4e+04; Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	QY 2 GCGCGCGCGCAGGGGG 18 Db 152 GCGCGCGCGCAGGGGG 136
RESULT 6 CNLS026IH	
LOCUS	CNS026IH linear GSS 01-SEP-2000
DEFINITION	Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 24IC17 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION	AL183410
VERSION	AL183410.1 GI:7821514
KEYWORDS	GSS: genome survey sequence.
SOURCE	Tetraodon nigroviridis
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE AUTHORS	
Ruest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J. Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000) 20296633	TITLE JOURNAL MEDLINE PUBLISHED PUBMED REFERENCE AUTHORS

ACCESSION CA757679
 VERSION CA757679.1 GI:25801718
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 577)
 AUTHORS Bohnert H.J., Borchert C., Brazille S., Brooks J., Eaton M., Ferrea H., Kawasaki S., McCollough A., Michalowski C.B., Palacio C., Scarpa G., Wheeler M. and Zepeda G.R.
 TITLE Functional Genomics of Plant Stress Tolerance
 JOURNAL Unpublished (2000)
 COMMENT Contact: Mark Fredrickson
 Department of Plant Biology
 University of Illinois
 1201 W. Gregory Dr., Urbana, IL 61801, USA
 Tel: 2172655473
 Email: bohnertlab@life.uiuc.edu

FEATURES
 source
 Location/Qualifiers
 1..577
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /strain="Pokkali"
 /db_xref="taxon:4530"
 /clone="O306P11-T3.ab1"
 /tissue_type="roots"
 /dev_stage="1 week"
 /clone_lib="OS"
 /note="2-3 d 150mM NaCl"

ORIGIN
 Query Match 91.1%; Score 16.4; DB 14; Length 577;
 Best Local Similarity 94.4%; Pred. No. 4e+04; 1; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCGCCGCGCGAGGGGG 18
 |||||
 DB 119 TGCGCCGCGCGAGGGGG 102
 |||||

RESULT 12
 CG852075 583 bp DNA linear GSS 18-NOV-2003
 LOCUS ZMWBB0343121.f ZMWBB Zea mays subsp. mays genomic clone
 DEFINITION ZMWBB0343121 5', genomic survey sequence.
 ACCESSION CG852075
 VERSION CG852075.1 GI:38378936
 KEYWORDS GSS.
 SOURCE Zea mays subsp. mays (maize)
 ORGANISM Zea mays subsp. mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 583)
 AUTHORS Yu Y., Kim H.R., Hatfield J., Soderlund C., Bharti A.K., Messing J. and Wing R.
 TITLE Sequencing of the maize genome
 JOURNAL Unpublished (2003)
 COMMENT Contact: Rod Wing
 Arizona Genomics Institute
 University of Arizona
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA
 Tel: 520 626 3967
 Fax: 520 621 9288
 Email: http://genome.arizona.edu
 PCR PRIMERs FORWARD: T7
 BACKWARD: M13r
 Plate: 0343 Row: I column: 21
 Seq primer: T7

Class: BAC ends.
 Location/Qualifiers
 1..583
 /organism="Zea mays subsp. mays"
 /mol_type="genomic DNA"
 /cultivar="B73"
 /sub_species="mays"
 /db_xref="taxon:4578"
 /clone="ZMWBB0343121"
 /lab_host="DH10B"
 /clone_lib="ZMWBB"
 /note="Vector: pBelosAC11; Site 1: HindIII; Site 2: HindIII; Zea mays L. ssp. mays"
 ORIGIN
 Query Match 91.1%; Score 16.4; DB 29; Length 583;
 Best Local Similarity 94.4%; Pred. No. 4e+04; 1; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCGCCGCGCGAGGGGG 18
 |||||
 DB 284 TGCGCCGCGCGAGGGGG 301
 |||||

RESULT 13
 BQ465952/c
 LOCUS HT01C12T HT Hordeum vulgare subsp. vulgare cDNA clone HT01C12
 DEFINITION 5-PRIME, mRNA sequence.
 ACCESSION BQ465952
 VERSION BQ465952.1 GI:21273734
 KEYWORDS EST.
 ORGANISM Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 660)
 AUTHORS Zhang H., Potokina E., Michalek W., Weschke W., Stein N. and Graner A.
 TITLE Barley ESTs from germinating seeds
 JOURNAL Unpublished (2002)
 COMMENT Contact: Stein Nils
 Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, 06466, Gatersleben, Germany
 Tel: 039482-5522
 Fax: 039482-5595
 Email: stein@ipk-gatersleben.de
 Insert length: 660 Std Error: 0.00
 Plate: 1 row: C column: 12
 Seq primer: T3
 Location/Qualifiers
 1..660
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="barke"
 /sub_species="vulgare"
 /db_xref="taxon:112509"
 /clone="HT01C12"
 /tissue_type="endosperm early"
 /dev_stage="0-16 hours after imbibition"
 /lab_host="XL10-Gold"
 /clone_lib="HT"
 /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

FEATURES
 source
 Location/Qualifiers
 1..660
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="barke"
 /sub_species="vulgare"
 /db_xref="taxon:112509"
 /clone="HT01C12"
 /tissue_type="endosperm early"
 /dev_stage="0-16 hours after imbibition"
 /lab_host="XL10-Gold"
 /clone_lib="HT"
 /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

ORIGIN

Query Match 91.1%; Score 16.4; DB 13; Length 660;
 Best Local Similarity 94.4%; Pred. No. 4e+04;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGCGCGCGCGCAGGGGG 18
 |||||
 Db 498 TGGCGCGCGCGCGGGGG 481

RESULT 14
 AL508223/c
 LOCUS
 DEFINITION AL508223 Hordeum vulgare Barke developing caryopsis (3-15.DAP)
 Hordeum vulgare subsp. vulgare cDNA clone HY08C05V 5', mRNA
 sequence.

ACCESSION AL508223.1 GI:12034438
 VERSION AL508223
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 671)
 AUTHORS Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.
 TITLE EST sequencing and analysis in barley
 JOURNAL Unpublished (2000)
 COMMENT Contact: Michalek W
 Institute for Plant Genetics and Crop Plant Research
 Corrensstr.3, D-06466 Gatersleben, Germany
 Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
 Seq primer: T3 primer for 5'end.

FEATURES
 source
 1..671
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="barke"
 /sub_species="vulgare"
 /db_xref="taxon:112509"
 /clone="HY08C05V"
 /tissue_type="developing caryopsis (3-15.DAP)"
 /lab_host="XLOLR"
 /clone_lib="XLOLR"
 /3-15.DAP"
 /note="Vector: plasmid pBK-CMV; Site 1: EcoRI; Site 2:
 XhoI; mRNA was made from developing Caryopsis (3-15.DAP)
 of spring barley variety 'Barke', a high quality malting
 variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI
 (3'-end of cDNA). NOTE: Due to a cloning artefact caused
 by the kit, in most cases the EcoRI site is NOT present,
 as well as the EcoRI adapter. Average insert size is 1 kb.
 Sequence trimming: Vector sequences and sequence ends were
 trimmed from the 5'- and 3'-end until a 50 bp window
 contains less than two ambiguities. The maximum length was
 set to 700 bp"

ORIGIN
 Query Match 91.1%; Score 16.4; DB 9; Length 671;
 Best Local Similarity 94.4%; Pred. No. 4e+04;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGCGCGCGCGCAGGGGG 18
 |||||
 Db 531 TGGCGCGCGCGCGGGGG 514

RESULT 15
 BQ466861/c
 LOCUS
 DEFINITION HS01N03T HS Hordeum vulgare subsp. vulgare cDNA clone HS01N03
 S-PRIME, mRNA sequence.
 ACCESSION BQ466861

VERSION BQ466861.1 GI:21274643
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 676)
 AUTHORS Zhang, H., Potokina, E., Michalek, W., Weschke, W., Stein, N. and
 Graner, A.
 TITLE Barley ESTs from germinating seeds
 JOURNAL Unpublished (2002)
 COMMENT Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, 06466, Gatersleben, Germany
 Tel: 039482-5522
 Fax: 039482-5595
 Email: stein@ipk-gatersleben.de
 Insert Length: 676 Std Error: 0.00
 Plate: 1 Row: N Column: 3
 Seq primer: T3

FEATURES
 source
 1..676
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="barke"
 /sub_species="vulgare"
 /db_xref="taxon:112509"
 /clone="HS01N03"
 /tissue_type="embryo + scutellum"
 /dev_stage="0-16 hours after imbibition"
 /lab_host="XL10-Gold"
 /clone_lib="HS"
 /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
 cDNA); Site 2: XhoI (3'-end of cDNA). Due to a cloning
 artefact caused by the kit, in most cases the EcoRI site
 is NOT present, as well as the EcoRI adapter used for
 cloning. To excise the insert, restriction sites upstream
 EcoRI should be used (e.g. BamHI, Sall, PstI). NOTE: Also
 due to the cloning system used Blue/white selection for
 recombinants is not 100% reliable."

ORIGIN
 Query Match 91.1%; Score 16.4; DB 13; Length 676;
 Best Local Similarity 94.4%; Pred. No. 4e+04;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGCGCGCGCGCAGGGGG 18
 |||||
 Db 526 TGGCGCGCGCGCGGGGG 509

Search completed: July 2, 2004, 13:33:05
 Job time : 1351.14 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:36:05 ; Search time 633.732 Seconds

(without alignments)
1231.080 Million cell updates/sec

Title: US-10-068-160-17

Perfect score: 18

Sequence: 1 tgcgcggcgccagggggg 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:**

1: gb_ba:**

2: gb_htg:**

3: gb_in:**

4: gb_om:**

5: gb_ov:**

6: gb_pat:**

7: gb_ph:**

8: gb_pl:**

9: gb_pr:**

10: gb_ro:**

11: gb_sts:**

12: gb_sy:**

13: gb_un:**

14: gb_vi:**

15: em_ba:**

16: em_fun:**

17: em_hum:**

18: em_in:**

19: em_mu:**

20: em_om:**

21: em_or:**

22: em_ov:**

23: em_pat:**

24: em_ph:**

25: em_pl:**

26: em_ro:**

27: em_sts:**

28: em_un:**

29: em_vi:**

30: em_htg_hum:**

31: em_htg_inv:**

32: em_htg_other:**

33: em_htg_mus:**

34: em_htg_pln:**

35: em_htg_rnd:**

36: em_htg_mam:**

37: em_htg_vrt:**

38: em_sy:**

39: em_htgo_hum:**

40: em_htgo_mus:**

41: em_htgo_other:**

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	17	94.4	1405	14	SHE581560	AJ581560 suid herp
C 2	17	94.4	232176	2	AC144804	AC144804 Gallus ga
C 3	16.4	91.1	816	8	AK122136	AK122136 Oryza sat
C 4	16.4	91.1	1655	8	AK060251	AK060251 Oryza sat
C 5	16.4	91.1	4225	10	AB017578	AB017578 Rattus no
C 6	16.4	91.1	4898	1	AY422718	AY422718 Pseudomon
C 7	16.4	91.1	5278	1	AB004065	AB004065 Pseudomon
C 8	16.4	91.1	96256	9	HS117715	AL022315 Human DNA
C 9	16.4	91.1	106117	9	AC103564	AC103564 Homo sapi
C 10	16.4	91.1	118436	8	AP005064	AP005064 Oryza sat
C 11	16.4	91.1	161617	9	AC093724	AC093724 Homo sapi
C 12	16.4	91.1	182944	2	AC133783	AC133783 Homo sapi
C 13	16.4	91.1	235115	2	AC133256	AC133256 Rattus no
C 14	16.4	91.1	235785	2	AC121480	AC121480 Rattus no
C 15	16	88.9	10029	1	AE008002	AE008002 Agrobacte
C 16	16	88.9	10029	1	AE009036	AE009036 Agrobacte
C 17	16	88.9	14952	1	SMJ4445	AE009036 Agrobacte
C 18	16	88.9	134940	2	AC018939	AC018939 Homo sapi
C 19	16	88.9	147984	2	AC141987	AC141987 Rattus no
C 20	16	88.9	176967	2	AC135864	AC135864 Oryza sat
C 21	16	88.9	300000	1	SM5591784	AL591784 Sinorhizo
C 22	15.4	85.6	852	11	PM3H12G	AL685751 Penicilli
C 23	15.4	85.6	885	8	BT005764	BT005764 Arabidops
C 24	15.4	85.6	887	8	AK107743	AK107743 Oryza sat
C 25	15.4	85.6	900	6	BD267140	BD267140 Compositi
C 26	15.4	85.6	969	6	AX654633	AX654633 Sequence
C 27	15.4	85.6	976	11	PM12D6G	AL684370 Penicilli
C 28	15.4	85.6	988	8	AK061421	AK061421 Oryza sat
C 29	15.4	85.6	1028	8	AK104181	AK104181 Oryza sat
C 30	15.4	85.6	1032	8	AK061195	AK061195 Oryza sat
C 31	15.4	85.6	1039	8	AK104630	AK104630 Oryza sat
C 32	15.4	85.6	1043	8	AK104655	AK104655 Oryza sat
C 33	15.4	85.6	1061	6	AX305960	AX305960 Sequence
C 34	15.4	85.6	1072	8	AF049888	AF049888 Oryza sat
C 35	15.4	85.6	1204	8	AK120540	AK120540 Oryza sat
C 36	15.4	85.6	1246	8	AK105338	AK105338 Oryza sat
C 37	15.4	85.6	1300	8	BT008959	BT008959 Triticum
C 38	15.4	85.6	1426	8	AK058296	AK058296 Oryza sat
C 39	15.4	85.6	1577	8	AK111436	AK111436 Oryza sat
C 40	15.4	85.6	1595	8	OS1A1COX	X85747 O.sativa mr
C 41	15.4	85.6	1605	8	AK109694	AK109694 Oryza sat
C 42	15.4	85.6	1637	8	D83391	D83391 Zea mays mr
C 43	15.4	85.6	1808	10	MMMB6	X99143 M.musculus
C 44	15.4	85.6	1820	10	RNU55179	U55179 Rattus norv
C 45	15.4	85.6	1841	9	HSAL32887	AJ132887 Homo sapi

ALIGNMENTS

RESULT 1
SHE581560/c
LOCUS SHE581560
DEFINITION suid herpesvirus 1 partial ORF1.2 and left end of unique long region.
ACCESSION AJ581560
VERSION AJ581560.1 GI:34368527
KEYWORDS ORF1.2; unique long region.
SOURCE Suid herpesvirus 1
ORGANISM Suid herpesvirus 1
Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.
REFERENCE 1
AUTHORS Klupp, B.G., Hengartner, C.J., Mettenleiter, T.C. and Enquist, L.W.
TITLE The complete annotated sequence of the pseudorabies virus genome

1405 bp DNA linear VRL 30-AUG-2003

```

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1405)
AUTHORS Klupp B.G.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-2003) Klupp B.G., Institute of Molecular Biology,
Greifswald - Insel Riems, GERMANY
FEATURES
source
1..1405
/organism="Suid herpesvirus 1"
/vision
/mol type="genomic DNA"
/strain="Kaplan"
/db xref="taxon:10345"
3..84
/note="inverted repeat of nt 442-523"
/rpt_type=INVERTED
156..251
/note="spaced direct imperfect repeats"
/rpt_type=DIRECT
/rpt_unit="156..183"
complement(443..523)
/note="inverted repeat of nt 3-84"
/rpt_type=INVERTED
529..655
/note="3 spaced imperfect repeats"
/rpt_type=DIRECT
/rpt_unit="529..566"
751..958
/rpt_type=DIRECT
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1252..1405
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ORIGIN
Query Match 94.4%; Score 17; DB 14; Length 1405;
Rest Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGCGCGCGCGAGGGG 17
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Db 1168 TGGCGCGCGCGAGGGG 1152

RESULT 2
AC144804/c
LOCUS AC144804 232176 bp DNA linear HTG 24-JUN-2003
DEFINITION Gallus gallus clone CH261-22A23, WORKING DRAFT SEQUENCE, 14 ordered
pieces.
ACCESSION AC144804
VERSION AC144804.1 GI:30962733
KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT.
SOURCE Gallus gallus (Chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 232176)
AUTHORS Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,

```

```

Peng, Z., Malinov, I. and Rubin, E.M.
Direct Submission
Unpublished
2 (bases 1 to 232176)
Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
Peng, Z., Malinov, I. and Rubin, E.M.
Direct Submission
Submitted (21-MAY-2003) Genome Sciences, Lawrence Berkeley National
Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
3 (bases 1 to 232176)
Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
Peng, Z., Malinov, I. and Rubin, E.M.
Direct Submission
Submitted (24-JUN-2003) Genome Sciences, Lawrence Berkeley National
Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA

Sequence Produced by Berkeley FGA
Web site: http://pga.lbl.gov
Center Code: PGABERK
Center Project Name: G104
Bac Clone Name: CH261-22A23

This sequence has been compared to sequences of other species
using Vista (http://www-gsd.lbl.gov/ISTA). The results can be
viewed at:
http://pga.lbl.gov/cgi-bin/search_cvcgd?type=ntvalue=SRBBF1

The order-orientation of the draft sequence was accomplished by
using:
Avid (http://baboon.math.berkeley.edu/mavid),
Lagan (http://lagan.stanford.edu/) and paired end information.

Funding agent: Programs for Genomic Applications (MHLBI)

Summary Statistics:
Sequencing vector: Plasmid: pUC18
Chemistry: Dye-terminator Big Dye
Assembly program: Phrap version 0.990329.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 1187: contig of 1187 bp in length
* 1188 1287: gap of unknown length
* 1288 12634: contig of 11347 bp in length
* 12635 12734: gap of unknown length
* 12735 16456: contig of 3722 bp in length
* 16457 16556: gap of unknown length
* 16557 26480: contig of 9924 bp in length
* 26481 26580: gap of unknown length
* 26581 29898: contig of 3318 bp in length
* 29899 29998: gap of unknown length
* 29999 36595: contig of 6597 bp in length
* 36596 36895: gap of unknown length
* 36896 39486: contig of 2791 bp in length
* 39487 39586: gap of unknown length
* 39587 42321: contig of 2735 bp in length
* 42322 42421: gap of unknown length
* 42422 116738: contig of 74317 bp in length
* 116739 116838: gap of unknown length
* 116839 159322: contig of 42484 bp in length
* 159323 159422: gap of unknown length
* 159423 177889: contig of 18367 bp in length
* 177890 177889: gap of unknown length
* 177890 181431: contig of 3542 bp in length
* 181432 181531: gap of unknown length
* 181532 229280: contig of 47749 bp in length
* 229281 229380: gap of unknown length

```

Tanaka,T., Tomaru,A., Toyota,T., Tsunoda,Y., Ueda,M., Waki,K.,
Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J.,
Yokawa,S. and Yoshimura,A.
Collection, mapping, and annotation of 28K full-length cDNA clones
from japonica rice
Unpublished
3 (bases 1 to 616)
Kikuchi,S.
Direct Submission
Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan [E-mail:skkikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007]
This clone is one of the 32K full-length cDNA clones from japonica
rice.
URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Nishiki,T.,
Ohneda,E., Yabagi,W., Suzuki,K., Ii,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,M. and Nakahama,Y.
FAIS Genome Sequencing & Analysis Group: Ohtsuki,Y., Iida,Y.,
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M.,
Kobayashi,M., Kodama,T., Kuroaki,T., Kusumegi,T., Lu,M.,
Masuda,H., Miura,Y., Mizuno,K., Narioka,R., Nikura,J., Oka,M.,
Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M.,
Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Hiraoka,T., Hori,P., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,
Ota,Y., Saitho,H., Sakai,C., Sakai,K.,
Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K.,
Shikazawa,A., Shiraki,T., Sogabe,Y., Tagami,M.,
Tagami-Takeda,Y., Tagawa,A., Takanashi,F.,
Takaku-Akaiira,S., Tanaka,T., Tomaru,A., Toyota,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="J033135J16"

ch 91.1%; Score 16.4; DB 8; Length 616;
Similarity 94.4%; Pred No. 8.2e+03;
17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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2 1 TGC GCG GCG GCG GCG GCG GCG GCG 207
|||||
3 1 TGC GCG GCG GCG GCG GCG GCG GCG 207
|||||

AK060251 1665 bp mRNA linear PLN 24-JUL-2003
Oryza sativa (japonica cultivar-group) cDNA clone:001-004-C03, full
insert sequence.
AK060251
FLI_CDNA; oligo-capping.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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* 229381 232176: contig of 2796 bp in length.
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ORIGIN
Query Match          94.4%; Score 17; DB 2; Length 232176;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCGCGGCGCAGGGGG 17
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Db 177704 TCGCGCGGCGCAGGGGG 177688

RESULT 3
AK122136/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone:J033135J16, full
insert sequence.
AK122136
AK122136.1 GI:37991782
FLI CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1

The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team,
Kikuchi S, Satoh K, Nagata T, Kawagashira N, Doi K,
Kishimoto N, Yarak J, Ishikawa M, Yamada H, Ooka H, Hotta I,
Kojima K, Namiki T, Ohneda E, Yahagi M, Suzuki K, Li C,
Ohtsuki K, Shishiki T, Foundation of Advancement of International
Science Genome Sequencing & Analysis Group, Otonari Y, Murakami K,
Iida Y, Sugano S, Fujimura T, Suzuki Y, Tsunoda Y,
Kurosaki T, Kodama T, Masuda H, Kobayashi M, Xie Q, Lu M,
Narikawa R, Sugiyama A, Mizuno K, Yokomizo S, Niikura J,
Ikeda R, Ishibiki J, Kawamata M, Yoshimura A, Miura J,
Kusumegi T, Oka M, Ryu R, Ueda M, Matsubara K, RIKEN,
Kawai J, Carninci P, Adachi J, Aizawa K, Arakawa T, Fukuda S,
Hara A, Hashidume M, Hayatsu N, Imotani K, Ishii Y, Itoh M,
Kagawa I, Kondo S, Konno H, Miyazaki A, Osato N, Ota Y,
Saito R, Sasaki D, Sato K, Shibata K, Shinagawa A, Shiraki T,
Yoshino M, and Hayashizaki Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)
12869764
2

Adachi J, Aizawa K, Akimura T, Arakawa T, Carninci P, Doi K,
Fujimura T, Fukuda S, Hanagaki T, Hara A, Hashizume W,
Hayashida K, Hayashizaki Y, Hayatsu N, Hiramoto K, Hiraoka T,
Hori F, Hotta I, Iida J, Iida Y, Ikeda R, Imamura K,
Imotani K, Ishibiki J, Ishii Y, Ishikawa M, Itoh M, Kagawa I,
Kanagawa S, Katoh H, Kawagashira N, Kawai J, Kawamata M,
Kikuchi S, Kishikawa-Hirozane T, Kishimoto N, Kobayashi M,
Kodama T, Kojima K, Kojima Y, Kondo S, Konno H, Kouda M,
Koya S, Kurahara C, Kurosaki T, Kusumegi T, Li C, Lu M,
Masuda H, Matsubara K, Matsuyama T, Miura J, Miyazaki A,
Mizuno K, Murakami K, Murata M, Nagata T, Nakahama Y,
Nakamura M, Namiki T, Narikawa R, Niikura J, Nishi K,
Nomura K, Numaaki R, Ohneda E, Ohno M, Ohtsuki K, Oka M,
Ooka H, Osato N, Ota Y, Otonari Y, Ryu R, Saitoh H, Sakai C,
Shibata K, Shinagawa A, Shiraki T, Shishiki T, Sogabe Y,
Sugano S, Sugiyama A, Suzuki K, Suzuki Y, Tagami M,
Tagami-Takeda Y, Tagawa A, Takahashi F, Takaku-Akashira S,

```

REFERENCE
AUTHORS

Ehrhartoidae; Oryzae; Oryza.

1 The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team:
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Tsunoda, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN,
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, N., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Oka, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M., and Hayashizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from

japonica rice

Science 301 (5631), 376-379 (2003)

22752273

12869764

2 (bases 1 to 1665)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T.,
Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Inamura, K., Kagawa, I.,
Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,
Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M.,
Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,
Mizuno, K., Murakami, K., Murakami, M., Nagata, T., Nakamura, M.,
Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K.,
Numasaki, R., Ohneda, E., Ohno, M., Ohsuki, K., Oka, M., Ooka, H.,
Osato, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K.,
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,
Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,
Tagawa, A., Takahashi, P., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,
Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
Yoshimura, A.

Direct Submission

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602 Japan (E-mail: shikuchi@nias.affrc.go.jp).

Tel: 81-29-839-7007, Fax: 81-29-838-7007

This clone is one of the 28K full-length cDNA clones from japonica
rice.

URL : <http://cdna01.dna.affrc.go.jp/cdna/>

NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohsuki, K., Shishiki, T. and
Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

TITLE
JOURNAL

COMMENT

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N.,
Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, P.,
Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A. and Hayashizaki, Y.
Location/Qualifiers
1. 1665
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="001-004-C03"

FEATURES
source

ORIGIN

Query Match: 91.1%; Score 16.4; DB 8; Length 1665;
Best Local Similarity 94.4%; Pred. No. 6.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCCTCCGCGCAGGGGG 18

Db 1338 TGCCTCCGCGCAGGGGAG 1321

RESULT 5

AB017578S1

LOCUS

AB017578S1 4225 bp DNA linear ROD 20-NOV-1999
Rattus norvegicus gene for cGMP-binding cGMP-specific
phosphodiesterase, exon1a, exon1b and 5'-flanking region.

ACCESSION

AB017578

VERSION

AB017578.1

KEYWORDS

cGMP-binding

SEGMENT

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES
source

exon

exon

ORIGIN

Query Match

91.1%; Score 16.4; DB 10; Length 4225;

Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGC GCGCGCGGCGAGGGGG 18
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Db 3447 TGC GCGCGCGGCGAGGGGG 3464

RESULT 6
AY422718/c
LOCUS
DEFINITION Pseudomonas sp. K82 catechol 2,3 gene cluster, partial sequence.
ACCESSION AY422718
VERSION AY422718.1 GI:37790591
KEYWORDS
SOURCE
ORGANISM Pseudomonas sp. K82
Pseudomonas sp. K82
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
REFERENCE
1 (bases 1 to 4898)
Kim,S.-I., Kim,J.-Y. and Kim,E.-A.
TITLE
Proteome analysis of aromatic compounds degrading bacterium,
Pseudomonas sp. K82
JOURNAL
REFERENCE
2 (bases 1 to 4898)
Kim,S.-I.
Direct Submission
TITLE
Submitted (25-SEP-2003) Proteome Analysis, Korea Basic Science
Institute, 52, Yeosu-Dong, Yusung-Ku, Daejeon 305-806, Korea
JOURNAL
FEATURES
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HLIAFLDSHVDVLSADVNAKTKTRIDVAPTRHGITRGETIYFFPDSGRNRTSAGL
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4247..54898
/codon_start=1
/transl_table=11
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/protein_id="AA03453.1"
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VAAGRAALKGEMTMSVVKRAELHAVADEINRRPDDFLAELADTGKPSLASHIDI
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MKVGPALACRQHQSSVKPSSETPATALLGEVNAVGVPKSGVPGNARLRPLGRRI"
Query Match 91.1%; Score 16.4; DB 1; Length 4898;
Best Local Similarity 94.4%; Pred. No. 5.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGC GCGCGCGGCGAGGGGG 18
||||| |||||||
Db 1519 TGC GCGCGCGGCGAGGGGG 1502

RESULT 7
AB004065/c
LOCUS
DEFINITION Pseudomonas sp. genes for ORF1, ORF2, ORF3, chloroplast-type
ferredoxin, catechol 2,3-dioxygenase, 2-hydroxymuconic
6-semialdehyde dehydrogenase, partial and complete cds.
ACCESSION AB004065 D86528
VERSION AB004065.1 GI:11610562
KEYWORDS 2-hydroxymuconic 6-semialdehyde dehydrogenase; catechol
2,3-dioxygenase; chloroplast-type ferredoxin; ORF3; ORF2; ORF1.
SOURCE Pseudomonas sp.
ORGANISM Bacteria; Proteobacteria.
REFERENCE
1
Murakami,S., Nakanishi,Y., Kodama,N., Takenaka,S., Shinke,R. and
Aoki,K.
TITLE
Purification, characterization, and gene analysis of catechol
2,3-dioxygenase from the aniline-assimilating bacterium Pseudomonas
species AW-2
JOURNAL Biosci. Biotechnol. Biochem. 62 (4), 747-752 (1998)
MEDLINE 98276889
PUBMED 9614705
REFERENCE 2 (bases 1 to 5278)
Murakami,S.
AUTHORS
Direct Submission
TITLE
Submitted (16-MAY-1997) Shuichi Murakami, Kobe University,
Department of Biofunctional Chemistry; 1-1 Rokkodai-cho, Nada-ku,

Kobe 657, Japan (E-mail:hakko2@kobe-u.ac.jp, Tel:81-78-803-0681,
 Fax:81-78-803-0680)
 D86528:Submitted (08-Jul-1996).
 Location/Qualifiers
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 FEL"
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 GIEPSRYRDPDGAALGAVETGAEGPDABLTQLKQHTVSVRGQQLLGAAMLDA
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 1390 2292
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 /evidence=not experimental
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 /db_xref="GI:11610565"
 /translations="MTRDGTTPPMDLIRAFALRHGVSVEVADMEGIDDLTPERI
 RVLEQRGRFLVRSSENGKASADLHALVSAACHMEARARSFQNGHAGVVRISLM
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 KIGAVAVGAYASRAYLARHDTASNFVDDHLLANLQGFQHDNFYALMDWAKF
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 2403 2678
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 /db_xref="GI:11610566"
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 2700 3644
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 2700 3644
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 /EC_number="1.13.11.2"
 /function="meta-cleavage of catechol"
 /codon_start=1
 /evidence=experimental
 /transl_table=11
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 /protein_id="BAB18933.1"
 /db_xref="GI:11610567"
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WDEWKYSVILTPSPDQAGNHLAYKVEKADLEALQOKIEAMGVKTTMLDEGLPSTG
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 AGINTVADNTRFMTALDFFLFEQVLVQPEGNMQAATWMAATTTTHDIAFVGGPSGL
 HIAFELDSHVDLKSADVMAKTRIDVAPTRHGI TRGETIYFPDPSNRNRTAGL
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 4245 4808
 /gene="alnG"
 /note="7 amino acids coded by Tns attached at C terminal."
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 /evidence=experimental
 /transl_table=11
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 /db_xref="GI:11610568"
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 4788 5278
 /note="transposon Tns-Mob"
 /organism="Escherichia coli"
 ORIGIN
 Query Match 91.1%; Score 16.4; DB 1; Length 5278;
 Best Local Similarity 94.4%; Pred. No. 5.3e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TCGCGCGGCGCAGGGGG 18
 |||||
 DB 1519 TCGCGCGGCGCAGGGTGG 1502
 RESULT 8
 HS117715 96256 bp DNA linear PRI 05-JUN-2003
 LOCUS Human DNA sequence from clone RPS-117715 on chromosome 22q13.1
 DEFINITION Contains a novel gene, the MS555 gene for serum constituent protein
 MSE55, the LGALS2 gene for soluble Galactose-binding Lectin 2
 (Galactin 2, S-lac Lectin 2, HL14), ESTs, an STS, GSSs and two
 putative CpG islands, complete sequence.
 ACCESSION AL022315
 VERSION AL022315.1 GI:3820991
 KEYWORDS HTG; CpG island; galactin; lectin; LGALS2; MSE55.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 96256)
 Coville,G.
 Direct Submission
 Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
 On Nov 2, 1998 this sequence version replaced gi:3550020.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em., ENBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
 on the WORMPEP database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep -----
 Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquery@sanger.ac.uk -----
 COMMENT
 On Nov 2, 1998 this sequence version replaced gi:3550020.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em., ENBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
 on the WORMPEP database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep -----
 Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquery@sanger.ac.uk -----


```

repeat_region 12557..12569
/notes="2.2 copies 6 mer GCGCTG 26% conserved"
repeat_region 12663..12697
/notes="5.8 copies 6 mer CTTCTT 70% conserved"
repeat_region 12763..12775
/notes="2.2 copies 6 mer TTGAGC 26% conserved"
repeat_region 13154..13168
/notes="AluX repeat: matches 1..308 of consensus"
repeat_region 13480..13747
/notes="AluYB repeat: matches 30..311 of consensus"
repeat_region 13760..13846
/notes="29.0 copies 3 mer GAG 77% conserved"
repeat_region 13762..13784
/notes="2.1 copies 11 mer GGAGGAGGAGG 46% conserved"
repeat_region 13779..13788
/notes="2.5 copies 4 mer GGAG 20% conserved"
repeat_region 13860..13880
/notes="2.5 copies 4 mer GGAG 20% conserved"

Query Match 91.1%; Score 16.4; DB 9; Length 96256;
Best Local Similarity 94.4%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCGCGCGCGCGGGG 18
Db 21755 TCGCGCGCGCGCGGGG 21772

RESULT 9
AC103564 106117 bp DNA linear PRI 23-MAR-2002
LOCUS Homo sapiens BAC clone RP11-788A1 from 2, complete sequence.
DEFINITION AC103564
ACCESSION AC103564
VERSION AC103564.5 GI:19482407
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 106117)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998);
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 106117)
AUTHORS VanBrunt,A., Kozlowski,A. and Spalding,L.
TITLE The sequence of Homo sapiens BAC clone RP11-788A1
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 106117)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (28-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 106117)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 106117)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 6 (bases 1 to 106117)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On Mar 15, 2002 this sequence version replaced gi:18677687.
----- Genome Center

```

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: sapiens@wustl.edu
----- Summary Statistics
Center project name: H_NH0788A01

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tatenio,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is AJ239322, 2000 bp overlap.
Actual start of this clone is at base position 1 of RP11-788A1.

Polymorphisms exist between AC103564, AC093724 and AJ239322. Data from AC093724 was used to finish AC103564.

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/chromosome="2"	
/map="2"	
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/clone_lib="RPCI-11"	
548..568	
repeat_region	/rpt_family="AT_rich"
669..1023	
misc_feature	/note="similar to Homo sapiens EST A1651841 (NID:G4735820)"
707..791	
repeat_region	/rpt_family="MIR"
954..960	
misc_feature	/note="similar to Homo sapiens EST A1824189 (NID:G5444860)"
wj07h03.x1"	
1331..1605	
repeat_region	/rpt_family="Alu"
1743..2012	
repeat_region	/rpt_family="Alu"
2213..2320	
repeat_region	/rpt_family="ERV1"
2451..2767	
repeat_region	/rpt_family="ERV1"
2772..2914	
repeat_region	/rpt_family="L1"
2915..3208	
repeat_region	

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3209. .3921
/rpt_family="L1"
repeat_region 4396. .5149
/rpt_family="L1"
repeat_region 5153. .5365
/rpt_family="ERV1"
repeat_region 5421. .5535
/rpt_family="ERV1"
repeat_region 5536. .5599
/rpt_family="ERV1"
misc_feature 5977. .6763
/note="match to EST BG221914 (NID:gl3747935)"
misc_feature 6031. .6813
/note="match to EST BG221911 (NID:gl3747932)"
repeat_region 6245. .6660
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repeat_region 6661. .7534
/rpt_family="MaLR"
repeat_region 7537. .8028
/rpt_family="ERV1"
repeat_region 8037. .8331
/rpt_family="Alu"
repeat_region 8359. .8990
/rpt_family="MaLR"
repeat_region 8993. .9386
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misc_feature 10006. .10226
/note="match to EST BP879314 (NID:gl2269444)"
misc_feature 10259. .10262
/note="match to EST BG221911 (NID:gl3747932)"
misc_feature 10284. .10707
/note="match to EST BG221795 (NID:gl3747816)"
repeat_region 10285. .10570
/rpt_family="Alu"
misc_feature 10701. .10707
/note="match to EST BG221794 (NID:gl3747815)"
repeat_region 10966. .10993
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repeat_region 11141. .11169
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misc_feature 11202. .11364
/note="match to EST BG221794 (NID:gl3747815)"
misc_feature 11202. .11364
/note="match to EST BG221795 (NID:gl3747816)"
misc_feature 11237. .11247
/note="similar to Homo sapiens EST AA453375 (NID:gl2167044)
zx47e02.r1"
repeat_region 11409. .11767
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repeat_region 12574. .12641
/rpt_family="MaLR"
repeat_region 12642. .12753
/rpt_family="Alu"
repeat_region 12762. .13191
/rpt_family="(TA)n"
repeat_region 13193. .13473
/rpt_family="Alu"
repeat_region 13528. .13596
/rpt_family="L2"
repeat_region 14116. .14329
/rpt_family="ERV1"
repeat_region 14474. .14586
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misc_feature 15168. .15188
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(NID:gl0821458)"
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zn55c01.sl"
15599. .15932
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15933. .16267
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16269. .16592
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16598. .17385
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Query Match 91.1%; Score 16.4; DB 9; Length 106117;
Best Local Similarity 94.4%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCGCGCGCGCGG 18
|||||
Db 24281 TCGCGCGCGCGCGG 24298
|||||

RESULT 10
AP005064/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 8,
BAC clone:OSUNBa0049G15, complete sequence.
ACCESSION
AP005064
VERSION
AP005064.2 GI:30984143
KEYWORDS
HTG.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1
AUTHORS
Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLES
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC
clone:OSUNBa0049G15
JOURNAL
Published Only in Database (2002)
REFERENCE
2 (bases 1 to 118436)
AUTHORS
Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLES
Direct Submission
JOURNAL
Submitted (11-APR-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program, Kamondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasakienias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT
On May 21, 2003 this sequence version replaced gi:20142142.
The orientation of the sequence is from -21M13 to M13rev of the BAC
clone.
FEATURES
source
Location/Qualifiers
1. .118436
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="8"
/clone="OSUNBa0049G15"

Query Match 91.1%; Score 16.4; DB 8; Length 118436;
Best Local Similarity 94.4%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCGCGCGCGCGG 18
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Db 28966 TCGCGCGCGCGCGG 28949
|||||

RESULT 11
AC093724
LOCUS
DEFINITION
Homo sapiens BAC clone RP11-1L5 from 2, complete sequence.
ACCESSION
AC093724
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VERSION      AC093724.3  GI:31194053
KEYWORDS     HTG.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 161617)
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLES       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL      Sulston, J.E. and Wilson, R.
MEDLINE      Toward a complete human genome sequence
PUBMED       Genome Res. 8 (11), 1097-1108 (1998)
99063792
9847074
REFERENCE    2 (bases 1 to 161617)
AUTHORS      Nguyen, C. and Kozlowski, A.
TITLES       The sequence of Homo sapiens BAC clone RP11-11L5
JOURNAL      Unpublished (2001)
REFERENCE    3 (bases 1 to 161617)
AUTHORS      Waterston, R.H.
TITLES       Direct Submission
JOURNAL      Submitted (10-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 161617)
Waterston, R.
Direct Submission
Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 161617)
Wilson, R.
Direct Submission
Submitted (30-MAY-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On May 30, 2003 this sequence version replaced gi:1903950.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.edu
----- Summary Statistics
Center project name: H_NH0001L05
Drafting Center: WIBR
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NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male
donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E.,
Tateno, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at http://www.chori.org
VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

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This sequence is the entire insert of the clone. This clone is overlapped by AC093838 and AC103564.

Bacterial transposon in unfinished region of the clone.

The sequence of AC012122 has been incorporated into AC093724.

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FEATURES
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            /map="2"
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            /clone_lib="RPCI-11"
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            2193..2386
                /rpt_family="L1"
            2828..3125
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            3261..3382
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            3383..3783
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            3784..4077
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            4078..5130
                /rpt_family="L1"
            5131..5186
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            5187..6400
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            6401..6421
                /rpt_family="(TA)n"
            6422..6447
                /rpt_family="ERV1"
            6450..6901
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                /rpt_family="MER2_type"
            7937..8029
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            8394..8622
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            9122..9278
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            10031..10316
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            11309..11415
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            11891..12048
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            12119..12402
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            12403..12561
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            12930..12950
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            15239..15296
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            16597..16893
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repeat_region 23547..23688
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rpt_family="ERVX"
repeat_region 25242..25264
rpt_family="AT_rich"
repeat_region 27124..27228
rpt_family="(CG)n"
repeat_region 27314..27342
rpt_family="(CCG)n"
repeat_region 27804..27826
rpt_family="AT_rich"
repeat_region 28216..28243
rpt_family="AT_rich"
repeat_region 28857..28898
rpt_family="(TG)n"
repeat_region 30012..30110
rpt_family="MIR"
repeat_region 30098..30294
rpt_family="MIR"
repeat_region 30335..30618
rpt_family="Mariner"
repeat_region 31418..31478
rpt_family="L2"
repeat_region 34032..34060
rpt_family="(T)n"
repeat_region 34406..34452
rpt_family="L2"
repeat_region 34554..34724
rpt_family="MIR"
repeat_region 35381..35728
rpt_family="Alu"
repeat_region 36183..36210
rpt_family="AT_rich"
repeat_region 36773..36795
rpt_family="AT_rich"
repeat_region 37271..37800
rpt_family="L2"
repeat_region 38115..38338
rpt_family="MER1_type"
repeat_region 39197..39231
rpt_family="AT_rich"
repeat_region 39360..39380
rpt_family="AT_rich"
repeat_region 39402..39429
rpt_family="AT_rich"
repeat_region 39944..39978
rpt_family="AT_rich"
repeat_region 40077..40106
rpt_family="AT_rich"
repeat_region 40549..40588
rpt_family="AT_rich"

Query Match 91.1%; Score 16.4; DB 9; Length 161617;
Best Local Similarity 94.4%; Pred.No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCGCGGCGCGAGGGGG 18
|||||
Db 105507 TGGCGCGGCGCTGGGGG 105524

RESULT 12
AC133783/C
LOCUS AC133783 182944 bp DNA linear HTG 18-SEP-2002
DEFINITION Homo sapiens chromosome 2 clone RP11-191D7, *** SEQUENCING IN
PROGRESS ***, 14 unordered pieces.
ACCESSION AC133783
VERSION AC133783.1 GI:23132694
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

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REFERENCE
AUTHORS
  Waterston,R.H.
TITLE
  The sequence of Homo sapiens clone
JOURNAL
  Unpublished
REFERENCE
AUTHORS
  Waterston,R.H.
TITLE
  Direct Submission
JOURNAL
  Submitted (18-SEP-2002) Genome Sequencing Center, Washington
  University School of Medicine, 4444 Forest Park Parkway, St. Louis,
  MO 63108, USA

```

COMMENT

```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0191D07
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-terminator ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 178033 bases at least Q40
Consensus quality: 179089 bases at least Q30
Consensus quality: 179748 bases at least Q20
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

```

```

* 1 1114: contig of 1114 bp in length
* 1115 1214: gap of unknown length
* 1215 2766: contig of 1552 bp in length
* 2767 2866: gap of unknown length
* 2867 4107: contig of 1241 bp in length
* 4108 4207: gap of unknown length
* 4208 5400: contig of 1193 bp in length
* 5401 5500: gap of unknown length
* 5501 6648: contig of 1148 bp in length
* 6649 6749: gap of unknown length
* 6749 8035: contig of 1286 bp in length
* 8035 8135: gap of unknown length
* 8135 9887: contig of 1752 bp in length
* 9887 9986: gap of unknown length
* 9987 13127: contig of 3141 bp in length
* 13128 13227: gap of unknown length
* 13228 20610: contig of 7383 bp in length
* 20611 20710: gap of unknown length
* 20711 31095: contig of 10385 bp in length
* 31096 31195: gap of unknown length
* 31196 40313: contig of 9118 bp in length
* 40314 40413: gap of unknown length
* 40414 68780: contig of 28367 bp in length
* 68781 68880: gap of unknown length
* 68881 108997: contig of 40117 bp in length
* 108998 109097: gap of unknown length
* 109098 182944: contig of 73847 bp in length.

```

FEATURES

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    /db_xref="taxon:9606"
    /chromosome="2"
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    /note="assembly_name:Contig16"
  1215..2766
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misc_feature

misc_feature

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misc_feature 4208. 5400 /note="assembly_name:Contig24"
misc_feature 5501. 6648 /note="assembly_name:Contig26"
misc_feature 6749. 8034 /note="assembly_name:Contig28"
misc_feature 8135. 9886 /note="assembly_name:Contig32"
misc_feature 9987. 13127 /note="assembly_name:Contig33"
misc_feature 13228. 20610 /note="assembly_name:Contig34"
misc_feature 20711. 31095 /note="assembly_name:Contig35"
misc_feature 31196. 40313 /note="assembly_name:Contig36"
misc_feature 40414. 68780 /note="assembly_name:Contig37"
misc_feature 68881. 108997 /note="assembly_name:Contig38"
misc_feature 109098. 162944 /note="assembly_name:Contig39"
misc_feature clone_end:SP6 vector_side:right"

ORIGIN
Query Match 91.1%; Score 16.4; DB 2; Length 182944;
Best Local Similarity 94.4%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCCTGGCGCGCAGGGGGG 18
Db 8872 TGCCTGGCGCGCTGGGGGG 8855

RESULT 13
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LOCUS AC133256 235115 bp DNA linear HTG 20-NOV-2002
DEFINITION Rattus norvegicus clone CH230-198G22, WORKING DRAFT SEQUENCE, 3
unordered pieces.
AC133256 AC133256.2 GI:25139160
VERSION HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 235115)
Muzny,D.,Marie., Metzker,M.,Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,J., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,V., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flegg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,A., Garcia,A., Garner,T., Garza,M.,
Gebrgeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Guraratne,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Haves,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howells,S., Hudlyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,

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Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
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Lorensukewa,L., Loulseghe,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindarine,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Mirja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokemele,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savary,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Stelmle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,R., Wiecezyk,R., Wooden,H., Worley,K.,
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Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 235115)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 235115)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KBQQ
Center clone name: CH230-198G22
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 213061 bases at least Q40
Consensus quality: 215965 bases at least Q30
Consensus quality: 217641 bases at least Q20
Estimated insert size: 214397; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).
* NOTE: This is a 'working draft' sequence. It currently

```


* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 232089: contig of 232089 bp in length
232090 232189: gap of unknown length
232190 233481: contig of 1292 bp in length
233482 233581: gap of unknown length
233582 235115: contig of 1534 bp in length.

Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clones="CH230-198G22"

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complement(8293..8848)
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site:
end_sequence:BH348925"

ORIGIN
Query Match 91.1%; Score 16.4; DB 2; Length 235115;
Best Local Similarity 94.4%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCGCCCGCGCAGGGGG 18
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Db 126991 TGCGCCCGCGCAGGGGG 126974
|||||

RESULT 14
AC121480/c
LOCUS
DEFINITION Rattus norvegicus clone CH230-517B22, *** SEQUENCING IN PROGRESS
*** 3 unordered pieces.
AC121480
AC121480.4 GI:25138141
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 235785)
Muzny, D., Marie, Metzker, M., Lee, S., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Altschul, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Ayoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buay, C., Burch, P., Burrell, K., Calderon, S.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Chen, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escoto, M., Eugene, C., Evans, C.A., Falls, I., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregiorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,

Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
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Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorenshuwa, L., Loulsegue, H., Lozano, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, B.,
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Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Mair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwaokemele, O., Okwuonu, G., Olarnunsaogoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,
Plopper, P., Poindexter, A., Popovic, D., Primus, E., Pu, L.,
Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,
Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
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Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
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Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 235785)
Worley, K.C.

Direct Submission
Submitted (18-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 235785)

Direct Submission
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:23907725.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GYD
Center clone name: CH230-517B22
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 204933 bases at least Q40
Consensus quality: 208631 bases at least Q30
Consensus quality: 210832 bases at least Q20

Estimated insert size: 211250; sum-of-contigs estimation
 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a "working draft" sequence. It currently
 * consists of 3 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 91766: contig of 91766 bp in length
 * 91767 91866: gap of unknown length
 * 91867 106790: contig of 14924 bp in length
 * 106791 106890: gap of unknown length
 * 106891 235785: contig of 128895 bp in length.

FEATURES
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 /db_xref="taxon:10116"
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 site:
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 /notes="wgs contig"
 79125..79167
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 clone_end:T7
 site:
 end_sequence:B2216212"
 91867..93348
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 clone_end:T7"
 93399..94986
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 106891..1108087
 /notes="wgs end_extension
 clone_end:T7"

misc_feature
 misc_feature
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 misc_feature

ORIGIN

Query Match 91.1%; Score 16.4; DB 2; Length 235785;
 Best Local Similarity 94.4%; Pred.No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGCGCGCAGGGGGG 18
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 Db 61071 TGGCGAGCGCGAGGGGGG 61054

RESULT 15
 AE008002/c
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 DEFINITION Agrobacterium tumefaciens str. C58 circular chromosome, section 60
 of 254 of the complete sequence.

ACCESSION AE008002 AE007869
 VERSION AE008002.1 GI:15155634

KEYWORDS
 SOURCE Agrobacterium tumefaciens str. C58 (Cereon)
 ORGANISM Agrobacterium tumefaciens str. C58 (Cereon)
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.

REFERENCE
 1 (bases 1 to 10029)
 Hinkle, G., Slater, S.C. and Goodner, B.
 Complete Genome Sequence of Agrobacterium tumefaciens C58
 (Rhizobium radiobacter C58), the Causative Agent of Crown Gall
 Disease in Plants

JOURNAL

REFERENCE 2 (bases 1 to 10029)

AUTHORS Hinkle, G., Slater, S.C. and Goodner, B.

TITLE Direct Submission

JOURNAL Submitted (14-AUG-2001) Cereon Genomics, 45 Sidney Street,

Cambridge, MA 02139, USA

FEATURES

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gene

CDS

JOURNAL

REFERENCE 2 (bases 1 to 10029)

AUTHORS Hinkle, G., Slater, S.C. and Goodner, B.

TITLE Direct Submission

JOURNAL Submitted (14-AUG-2001) Cereon Genomics, 45 Sidney Street,

Cambridge, MA 02139, USA

FEATURES

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GAGKSDIEGRVAGIKAQIBETTSDDYDREKLQERLAKLGGVAVIRVGGSTEVEVREK
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7919..8767
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/codon_start=1
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8825..9805
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ORIGIN
Query Match 38.9%; Score 16; DB 1; Length 10029;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGGCGCGCGCGCGCGG 16
Db 8449 TGGCGCGCGCGCGCGG 8434
Search completed: July 2, 2004, 10:08:07
Job time : 637.732 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 06:05:50 ; Search time 134.89 Seconds
(without alignments)
566.887 Million cell updates/sec

Title: US-10-068-160-17

Perfect score: 18

Sequence: 1 tgcgcggcgaggggggg 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseq1990s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001as:*

5: Geneseq2001bs:*

6: Geneseq2002s:*

7: Geneseq2003as:*

8: Geneseq2003bs:*

9: Geneseq2003cs:*

10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	20	7	ACC48302
2	15.4	85.6	374	4	AAL10608
3	15.4	85.6	450	4	AAL17683
4	15.4	85.6	499	3	AAC41286
5	15.4	85.6	900	3	AAAT9481
6	15.4	85.6	969	3	ADA71180
7	15.4	85.6	1008	3	AAC56198
8	15.4	85.6	1061	6	AB199675
9	15.4	85.6	1250	9	ADBO7415
10	15.4	85.6	1404	7	ACA42729
11	15.4	85.6	1611	9	ADDA49064
12	15.4	85.6	2196	7	ADAA59886
13	15.4	85.6	2448	9	ADD29815
14	15.4	85.6	2478	3	AAA79707
15	15.4	85.6	2559	9	ADD15216
16	15.4	85.6	2787	5	ABV21138
17	15.4	85.6	2929	5	ABV25833
18	15.4	85.6	2929	5	ABV29359
19	15.4	85.6	2929	5	ABV25524
20	15.4	85.6	2929	5	ABV28091
21	15.4	85.6	2929	5	ABV28883
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23	15.4	85.6	2929	5	ABV24150

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C 25	15.4	85.6	2929	5	ABV25159	Abv25159 Human pro
C 26	15.4	85.6	2929	5	ABV23047	Abv23047 Human pro
C 27	15.4	85.6	2929	5	ABV23269	Abv23269 Human pro
C 28	15.4	85.6	2929	5	ABV25226	Abv25226 Human pro
C 29	15.4	85.6	2929	5	ABV28062	Abv28062 Human pro
C 30	15.4	85.6	2929	5	ABV29113	Abv29113 Human pro
C 31	15.4	85.6	2929	5	ABV25353	Abv25353 Human pro
C 32	15.4	85.6	3104	7	ADA53342	Ada53342 Human cod
C 33	15.4	85.6	3179	4	AAD09560	Aad09560 Human tra
C 34	15.4	85.6	3364	4	AAK69788	Aak69788 Human imm
C 35	15.4	85.6	3517	6	AAK98307	Aak98307 Human pro
C 36	15.4	85.6	3917	6	AAK98308	Aak98308 Human pro
C 37	15.4	85.6	3918	6	AAK98309	Aak98309 Human pro
C 38	15.4	85.6	3918	6	AAK98317	Aak98317 Human pro
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C 40	15.4	85.6	3918	6	AAK98306	Aak98306 Human pro
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C 42	15.4	85.6	3918	6	AAK98315	Aak98315 Human pro
C 43	15.4	85.6	3918	6	AAK98314	Aak98314 Human pro
C 44	15.4	85.6	3918	6	AAK98313	Aak98313 Human pro
C 45	15.4	85.6	3918	6	AAK98318	Aak98318 Human pro

ALIGNMENTS

RESULT 1

ACC48302

ID ACC48302 standard; DNA; 20 BP.

XX

AC ACC48302;

XX

DT 11-AUG-2003 (first entry)

XX

DE Cpg oligodeoxynucleotide used for dendritic cell maturation.

XX

KW Cpg oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine; cytostatic; immunostimulant; gene therapy; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT misc_difference 1

FT /*tag= a

FT /note= "N is any base (especially G) or no base"

FT misc_difference 2

FT /*tag= b

FT /note= "N is any base (especially G) or no base"

XX

PN WO2003020884-A2.

XX

PD 13-MAR-2003.

XX

PF 13-AUG-2002; 2003WO-US025732.

XX

PR 14-AUG-2001; 2001US-03121902.

XX

{USSH } US DEPT HEALTH & HUMAN SERVICES.

XX

PI Kliman DM, Gursel M, Verthelyi D;

XX

DR WPI; 2003-300874/29.

XX

Generating mature dendritic cells for tumor immunotherapy or as vaccines for activating the immune system to treat diseases such as cancer, comprises contacting a dendritic cell precursor with a D type oligodeoxynucleotide.

XX

PS Disclosure; Page 26; 69pp; English.

XX

The present sequence is that of a D type Cpg oligodeoxynucleotide that is an example of claimed D type oligodeoxynucleotides (see ACC48294) of the

CC invention. Mature dendritic cells are obtained by contacting a dendritic
 CC cell precursor, such as a monocyte, with such an oligodeoxynucleotide.
 CC The method is useful for generating mature dendritic cells and enhancing
 CC T cell responses, thus enhancing antigen presentation. Mature dendritic
 CC cells are useful for tumour immunotherapy, for augmenting an immune
 CC response to an infectious agent or to a vaccine, and as vaccines to
 CC prevent future infection or to activate the immune system to treat
 CC diseases such as cancer. Mature dendritic cells may also be used to
 CC produce activated T lymphocytes

XX Sequence 20 BP; 1 A; 5 C; 11 G; 1 T; 0 U; 2 Other;

Query Match 100.0%; Score 18; DB 7; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGCCGGCGCAGGGGG 18

Db 3 TGCGCCGGCGCAGGGGG 20

RESULT 2

AAL10608/c

ID AAL10608 standard; cDNA; 374 BP.

XX AC

XX AAL10608;

XX DT 07-DEC-2001 (first entry)

XX DE Human breast cancer expressed polynucleotide 3065.

XX KW Human; breast cancer; cell marker; cytostatic; ss.

XX OS Homo sapiens.

XX PN WO200151628-A2.

XX PD 19-JUL-2001.

XX PF 10-JAN-2001; 2001WO-US000798.

XX PR 14-JAN-2000; 2000US-0176077P.

XX PR 14-MAR-2000; 2000US-0189167P.

XX PR 24-MAR-2000; 2000US-0192099P.

XX PR 29-MAR-2000; 2000US-0193480P.

XX PR 15-MAY-2000; 2000US-0205230P.

XX PR 09-JUN-2000; 2000US-0211315P.

XX PR 25-JUL-2000; 2000US-0220534P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Lillie J, Xu Y, Wang Y, Steinmann K;

XX DR WPI; 2001-451856/48.

XX PT New peptide useful as a marker for the diagnosis of breast cancer.

XX PS Claim 1; Page 569; 3695pp; English.

XX CC The invention relates to human breast cancer expressed polynucleotides
 CC (AAL07544-AAL26789) and methods of assessing whether a patient is
 CC afflicted with breast cancer by examining the correlation between the
 CC expression of certain markers and the cancerous state of breast cells.
 CC The polynucleotides and encoded polypeptides are potential markers for
 CC detecting, diagnosing, monitoring, characterising treating and
 CC potentially preventing breast cancer. The polynucleotides and encoded
 CC polypeptides are also useful for isolating compounds with cytostatic
 CC activity

XX SQ Sequence 374 BP; 69 A; 109 C; 122 G; 68 T; 0 U; 6 Other;

Query Match

Best Local Similarity 85.6%; Score 15.4; DB 4; Length 374;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGCCGGCGCAGGGGG 18

Db 304 GCGCCGGCGCAGGGGG 288

RESULT 3

AAL17683/c

ID AAL17683 standard; cDNA; 450 BP.

XX AC

XX AAL17683;

XX DT 07-DEC-2001 (first entry)

XX DE Human breast cancer expressed polynucleotide 10140.

XX KW Human; breast cancer; cell marker; cytostatic; ss.

XX OS Homo sapiens.

XX PN WO200151628-A2.

XX PD 19-JUL-2001.

XX PF 10-JAN-2001; 2001WO-US000798.

XX PR 14-JAN-2000; 2000US-0176077P.

XX PR 14-MAR-2000; 2000US-0189167P.

XX PR 24-MAR-2000; 2000US-0192099P.

XX PR 29-MAR-2000; 2000US-0193480P.

XX PR 15-MAY-2000; 2000US-0205230P.

XX PR 09-JUN-2000; 2000US-0211315P.

XX PR 25-JUL-2000; 2000US-0220534P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Lillie J, Xu Y, Wang Y, Steinmann K;

XX DR WPI; 2001-451856/48.

XX PT New peptide useful as a marker for the diagnosis of breast cancer.

XX PS Claim 1; Page 1809; 3695pp; English.

XX CC The invention relates to human breast cancer expressed polynucleotides
 CC (AAL07544-AAL26789) and methods of assessing whether a patient is
 CC afflicted with breast cancer by examining the correlation between the
 CC expression of certain markers and the cancerous state of breast cells.
 CC The polynucleotides and encoded polypeptides are potential markers for
 CC detecting, diagnosing, monitoring, characterising treating and
 CC potentially preventing breast cancer. The polynucleotides and encoded
 CC polypeptides are also useful for isolating compounds with cytostatic
 CC activity

XX SQ Sequence 450 BP; 83 A; 138 C; 146 G; 83 T; 0 U; 0 Other;

Query Match

Best Local Similarity 85.6%; Score 15.4; DB 4; Length 450;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGCCGGCGCAGGGGG 18

Db 260 GCGCCGGCGCAGGGGG 244

RESULT 4

AAC41286/c

ID AAC41286 standard; DNA; 499 BP.

XX AC

XX AAC41286;

XX DT 17-OCT-2000 (first entry)

XX Zea may DNA fragment SEQ ID NO: 31332.
 DE Hybridisation assay; genetic mapping; gene expression control;
 XX protein identification; signal transduction pathway; metabolic; pathway;
 KW promoter; termination sequence; corn; ss.
 XX Zea may subsp. may.
 OS
 XX
 PN EP1033405-A2.
 XX
 XX 06-SEP-2000.
 PD
 XX
 XX 25-FEB-2000; 2000EP-00301439.
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 XX 25-FEB-1999; 99US-0121825P.
 PR 05-MAR-1999; 99US-0121810P.
 PR 09-MAR-1999; 99US-0123548P.
 PR 23-MAR-1999; 99US-0125788P.
 PR 25-MAR-1999; 99US-0126264P.
 PR 29-MAR-1999; 99US-0126785P.
 PR 01-APR-1999; 99US-0127462P.
 PR 06-APR-1999; 99US-0128234P.
 PR 08-APR-1999; 99US-0128714P.
 PR 16-APR-1999; 99US-0128845P.
 PR 19-APR-1999; 99US-0130077P.
 PR 21-APR-1999; 99US-0130449P.
 PR 23-APR-1999; 99US-0130510P.
 PR 28-APR-1999; 99US-0130891P.
 PR 30-APR-1999; 99US-0131449P.
 PR 04-MAY-1999; 99US-0132407P.
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 PR 07-MAY-1999; 99US-0132487P.
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 PR 24-MAY-1999; 99US-0135353P.
 PR 25-MAY-1999; 99US-0135623P.
 PR 27-MAY-1999; 99US-0136021P.
 PR 28-MAY-1999; 99US-0136392P.
 PR 01-JUN-1999; 99US-0136782P.
 PR 03-JUN-1999; 99US-0137223P.
 PR 04-JUN-1999; 99US-0137528P.
 PR 07-JUN-1999; 99US-0137502P.
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 PR 18-JUN-1999; 99US-0139492P.
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 PR 18-JUN-1999; 99US-0139763P.
 PR 21-JUN-1999; 99US-0139817P.
 PR 22-JUN-1999; 99US-0139899P.
 PR 23-JUN-1999; 99US-0140353P.
 PR 24-JUN-1999; 99US-0140354P.
 PR 28-JUN-1999; 99US-0140695P.
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 PR 01-JUL-1999; 99US-0141287P.
 PR 01-JUL-1999; 99US-0141842P.
 PR 02-JUL-1999; 99US-0142154P.
 PR 06-JUL-1999; 99US-0142390P.
 PR 08-JUL-1999; 99US-0142803P.
 PR 09-JUL-1999; 99US-0142920P.
 PR 12-JUL-1999; 99US-0142977P.
 PR 13-JUL-1999; 99US-0143542P.
 PR 14-JUL-1999; 99US-0143624P.
 PR 15-JUL-1999; 99US-0144005P.
 PR 16-JUL-1999; 99US-0144085P.
 PR 19-JUL-1999; 99US-0144086P.
 PR 19-JUL-1999; 99US-0144325P.
 PR 19-JUL-1999; 99US-0144331P.
 PR 19-JUL-1999; 99US-0144332P.
 PR 19-JUL-1999; 99US-0144333P.
 PR 19-JUL-1999; 99US-0144334P.
 PR 20-JUL-1999; 99US-0144335P.
 PR 20-JUL-1999; 99US-0144632P.
 PR 20-JUL-1999; 99US-0144884P.
 PR 21-JUL-1999; 99US-0144814P.
 PR 21-JUL-1999; 99US-0145086P.
 PR 21-JUL-1999; 99US-0145088P.
 PR 22-JUL-1999; 99US-0145087P.
 PR 22-JUL-1999; 99US-0145089P.
 PR 22-JUL-1999; 99US-0145132P.
 PR 23-JUL-1999; 99US-0145145P.
 PR 23-JUL-1999; 99US-0145218P.
 PR 23-JUL-1999; 99US-0145224P.
 PR 26-JUL-1999; 99US-0145276P.
 PR 27-JUL-1999; 99US-0145913P.
 PR 27-JUL-1999; 99US-0145918P.
 PR 27-JUL-1999; 99US-0145919P.
 PR 28-JUL-1999; 99US-0145951P.
 PR 02-AUG-1999; 99US-0146386P.
 PR 02-AUG-1999; 99US-0146388P.
 PR 02-AUG-1999; 99US-0146389P.
 PR 03-AUG-1999; 99US-0147038P.
 PR 04-AUG-1999; 99US-0147204P.
 PR 05-AUG-1999; 99US-0147302P.
 PR 05-AUG-1999; 99US-0147192P.
 PR 06-AUG-1999; 99US-0147260P.
 PR 06-AUG-1999; 99US-0147303P.
 PR 06-AUG-1999; 99US-0147416P.
 PR 09-AUG-1999; 99US-0147493P.
 PR 09-AUG-1999; 99US-0147935P.
 PR 10-AUG-1999; 99US-0148171P.
 PR 11-AUG-1999; 99US-0148319P.
 PR 12-AUG-1999; 99US-0148341P.
 PR 13-AUG-1999; 99US-0148565P.
 PR 13-AUG-1999; 99US-0148684P.
 PR 16-AUG-1999; 99US-0149368P.
 PR 17-AUG-1999; 99US-0149175P.
 PR 18-AUG-1999; 99US-0149426P.
 PR 20-AUG-1999; 99US-0149722P.
 PR 20-AUG-1999; 99US-0149723P.
 PR 20-AUG-1999; 99US-0149929P.
 PR 23-AUG-1999; 99US-0149902P.
 PR 23-AUG-1999; 99US-0149930P.
 PR 25-AUG-1999; 99US-0150566P.
 PR 26-AUG-1999; 99US-0150884P.
 PR 27-AUG-1999; 99US-0151065P.
 PR 27-AUG-1999; 99US-0151066P.

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PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 16-SEP-1999; 99US-0154018P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155179P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 06-OCT-1999; 99US-0157753P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159328P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 18-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 22-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161320P.
PR 28-OCT-1999; 99US-0161392P.
PR 28-OCT-1999; 99US-0161393P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 85.6%; Score 15.4; DB 3; Length 499;
Best Local Similarity 94.1%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCGCGCGCGGGGG 18
DB 166 GCGCGCGCGCGGGGG 150

RESULT 5
AAA79481/c
ID AAA79481 standard; cDNA; 900 BP.
XX
AC AAA79481;
XX
DT 27-NOV-2000 (first entry)
XX
XX Eucalyptus grandis cell signalling involved polynucleotide SEQ ID NO:282.
XX
XX Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification;
XX plant cell signalling; modulation; transgenic plant; pathogen; growth;
XX environmental change; development; cell proliferation; differentiation;
XX elongation; survival; disease resistance; nutrient metabolism; ss.

PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 16-SEP-1999; 99US-0154018P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155179P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 06-OCT-1999; 99US-0157753P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159328P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 18-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 22-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161320P.
PR 28-OCT-1999; 99US-0161392P.
PR 28-OCT-1999; 99US-0161393P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 85.6%; Score 15.4; DB 3; Length 499;
Best Local Similarity 94.1%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCGCGCGCGGGGG 18
DB 166 GCGCGCGCGCGGGGG 150

RESULT 6
ADA71180/c
ID ADA71180 standard; DNA; 969 BP.
XX
AC ADA71180;
XX
DT 20-NOV-2003 (first entry)
XX
XX Rice gene, SEQ ID 4503.
XX
XX Plant; bacterial infection; fungal infection; viral infection; rice;
XX gene; ds.
XX
XX Oryza sativa.
XX
XX WO2003000898-A1.
XX
XX 03-JAN-2003.
XX
XX 22-JUN-2001; 2001WO-IB001105.

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XX Eucalyptus grandis.

XX WO200042171-A1.

XX 20-JUL-2000.

XX 11-JAN-2000; 2000WO-US000724.

XX 12-JAN-1999; 99US-00288986.

XX 01-NOV-1999; 99US-0162866P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Strabala TJ, Nieuwenhuizen NJ;

XX WPI; 2000-476052/41.

XX Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses to external signals.

XX Claim 1; Page 149; 527pp; English.

XX AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide and protein sequences isolated from eucalyptus (Eucalyptus grandis) or pine (Pinus radiata also known as Monterey pine). The protein sequences are involved in cell signalling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and development of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival, resistance to disease and nutrient metabolism. Examples of modifications which can be produced are altered fruit ripening and senescence of leaves and flowers e.g. to delay senescence and prolong the life of cut flowers or enhance senescence of reproductive organs to engineer sterile plants. Other modifications can be used to delay senescence in selected cell types or organs providing fruit and vegetables which have a longer shelf life between harvest and consumption, or to decrease branching frequency in forest tree species giving long stretches of valuable knot-free clear wood which can be used in solid timber furniture and veneers

XX Sequence 900 BP; 130 A; 375 C; 205 G; 130 T; 0 U; 0 Other;

XX Query Match 85.6%; Score 15.4; DB 3; Length 900;

XX Best Local Similarity 94.1%; Pred. No. 1.8e+03;

XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCGCGCGCGGGGG 18

DB 243 GCGCGCGCGCGGGGG 227

RESULT 6

ADA71180/c

ID ADA71180 standard; DNA; 969 BP.

XX AC

XX ADA71180;

XX DT 20-NOV-2003 (first entry)

XX XX Rice gene, SEQ ID 4503.

XX DE

XX Plant; bacterial infection; fungal infection; viral infection; rice;

XX gene; ds.

XX OS

XX Oryza sativa.

XX XX WO2003000898-A1.

XX XX 03-JAN-2003.

XX XX 22-JUN-2001; 2001WO-IB001105.

XX 22-JUN-2001; 2001WO-IB001105.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
XX Katagiri F, Quan S, Rao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX WPI; 2003-175290/17.
XX Identifying at least one gene involved in plant resistance or response to
XX pathogenic infection for conferring resistance or tolerance to a plant to
XX bacterial, fungal or viral infection by determining or detecting plant
XX gene expression.
XX Claim 6; SEQ ID NO 4503; 899pp; English.
XX The present invention relates to a method (M1) for identifying genes
XX involved in plant resistance or response to pathogenic infection. M1
XX comprises identifying a gene whose expression is significantly altered in
XX the incompatible interaction of plant gene expression relative to
XX expression of the gene in an uninfected plant, in a mutant plant that
XX does not express a gene associated with response to pathogenic infection,
XX or in a corresponding incompatible or compatible interaction. (M1) is
XX useful for conferring resistance to resistance or tolerance to a plant to
XX bacterial, fungal or viral infection. The present sequence was used to
XX illustrate the invention.
XX Sequence 969 BP; 196 A; 312 C; 309 G; 150 T; 0 U; 2 Other;
XX Query Match 85.6%; Score 15.4; DB 7; Length 969;
XX Best Local Similarity 94.1%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GCCTCCGCGCGAGGGGG 18
Db 811 GCCTCCGCGCGAGGGGG 795
RESULT 7
AAC56198/c
ID AAC56198 standard; DNA; 1008 BP.
XX AAC56198;
XX 25-JAN-2001 (first entry)
XX Eucalyptus grandis transcription factor DNA sequence #329.
XX Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
XX poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;
XX basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
XX homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
XX type 2 Cys2His2; CCAAT box element; MYB; ss.
XX Eucalyptus grandis.
XX WO200053724-A2.
XX 14-SBP-2000.
XX 09-MAR-2000; 2000WO-US006112.
XX 11-MAR-1999; 99US-00266513.
XX 18-AUG-1999; 99US-0149485P.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX Wood M, McGrath A, Shenk MA, Glenn M;
XX WPI; 2000-579369/54.
XX

PT New isolated polynucleotide encoding a plant transcription factor for
PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
PT having modified gene expression or modified activity of a polypeptide.
XX Claim 1; Page 131; 747pp; English.
XX The present invention relates to novel plant transcription factors from
XX Eucalyptus grandis or Pinus radiata. The present sequence is the coding
XX sequence for one such transcription factor. The transcription factor may
XX be used to produce a plant having modified gene expression such as a
XX woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or
XX mahogany species or to modify the activity of a polypeptide in a plant.
XX The transcription factors of the present invention are members from the
XX following families of regulatory proteins: bZIP, bZIP family of G-box
XX binding factors, basic helix-loop-helix zipper,
XX homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2
XX and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements and
XX MYB
XX Sequence 1008 BP; 175 A; 315 C; 331 G; 187 T; 0 U; 0 Other;
XX Query Match 85.6%; Score 15.4; DB 3; Length 1008;
XX Best Local Similarity 94.1%; Pred. No. 1.7e+03;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GCCTCCGCGCGAGGGGG 18
Db 236 GCCTCCGCGCGAGGGGG 220
RESULT 8
ABI99675
ID ABI99675 standard; cDNA; 1061 BP.
XX ABI99675;
XX 07-MAR-2002 (first entry)
XX Mouse ischaemic condition related cDNA sequence SEQ ID NO:711.
XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
XX vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX Mus musculus.
XX WO200188188-A2.
XX 22-NOV-2001.
XX 18-MAY-2001; 2001WO-JF004192.
XX 18-MAY-2000; 2000JP-00145977.
XX (UYNT-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX WPI; 2002-034733/04.
XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
XX expression levels of particular genes defined in the specification or by
XX determining the expression profile of a gene group comprising these
XX genes.
XX Claim 2; Page 1768-1769; 2690pp; English.
XX The present invention describes a method for examining ischaemic
XX conditions, comprising measuring the expression levels of particular
XX genes (I) in a test sample or determining the expression profile of a
XX gene group in the sample comprising genes selected from (I). The method
XX is useful for examining the ischaemic condition (e.g. compressive
XX ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
XX expression levels of particular genes (ABI99202 to ABI99912, encoding the

CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention

XX
 SQ Sequence 1061 BP; 177 A; 284 C; 405 G; 191 T; 0 U; 4 Other;

Query Match 85.6%; Score 15.4; DB 6; Length 1061;
 Best Local Similarity 94.1%; Pred. No. 1.7e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGCGCGCGCGAGGGGG 18
 |||||
 Db 891 GCGCGCGCGCGAGGGGG 907

RESULT 9

ADE07415

ID ADE07415 standard; DNA; 1250 BP.

AC ADE07415;

DT 29-JAN-2004 (first entry)

XX Novel coding sequence (useful for identifying genetic disorders) #481.

DE novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; Genetic disorder; gene; ds.

XX Unidentified.

XX #02003054152-A2.

PN #02003054152-A2.

XX 03-JUL-2003.

XX 10-DEC-2002; 2002WO-US039555.

XX 10-DEC-2001; 2001US-0339739P.

PR 11-DEC-2001; 2001US-0339453P.

PR 14-MAR-2002; 2002US-0365091P.

PR 14-MAR-2002; 2002US-0365384P.

PR 12-APR-2002; 2002US-0372381P.

PR 12-APR-2002; 2002US-0372615P.

PR 22-APR-2002; 2002US-00128558.

PR 24-APR-2002; 2002US-0376045P.

XX (HYSE-) HYSEQ INC.

PA Targ YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;

XX Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;

PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;

PI WPI; 2003-569235/53.

DR P-PSDB; ADE08326.

XX New polynucleotides, useful for expressing recombinant proteins for

PT analysis, characterization or therapeutic use, or as markers for tissues

PT in which the corresponding protein is preferentially expressed.

XX Claim 1; SEQ ID NO 481; 1177pp; English.

XX The invention comprises the amino acid and coding sequences of novel

CC proteins. The DNA and protein sequences of the invention are useful as:

CC markers for tissues in which the corresponding protein is preferentially

CC expressed; as molecular weight markers on gels; as chromosome markers or

CC tags; to identify chromosomes or to map related gene positions; and to

CC compare with endogenous DNA sequences in patients to identify potential

CC genetic disorders. The present DNA sequence represents a gene of the

CC invention.

XX

SQ Sequence 1250 BP; 202 A; 407 C; 419 G; 222 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 9; Length 1250;
 Best Local Similarity 94.1%; Pred. No. 1.7e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGCGCGCGCGAGGGGG 18
 |||||
 Db 72 GCGCGCGCGCGAGGGGG 88

RESULT 10

ACA42729

ID ACA42729 standard; DNA; 1404 BP.

XX ACA42729;

XX 19-JUN-2003 (first entry)

XX Prokaryotic essential gene #24386.

XX Antisense; ds; prokaryotic essential gene; cell proliferation;
 KW drug design; gene.

XX Pseudomonas aeruginosa.

XX #0200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JM;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR P-PSDB; ABU38859.

XX New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX Claim 14; SEQ ID NO 30599; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC the gene product or that has an activity against a biological pathway

CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1404 BP; 166 A; 458 C; 484 G; 296 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 7; Length 1404;

Best Local Similarity 94.1%; Pred. No. 1.7e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCGCGCGCGCGCGGG 17

Db 1154 TGCGCGCGCGCGCGGG 1170

RESULT 11

ADDA49064

ID ADD49064 standard; DNA; 1611 BP.

XX AC ADD49064;

XX DT 15-JAN-2004 (first entry)

XX DE Human NOV9b coding sequence, SEQ ID 37.

XX KW Antidiabetic; anorectic; cardiatic; hypotensive; antiarteriosclerotic;
 KW Virucide; antibacterial; fungicide; protozoacide; neurotropic;
 KW neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;
 KW antihypertensive; antiinflammatory; dermatological; antiasthmatic;
 KW antilipemic; gene therapy; NOV protein; metabolic disorder; diabetes;
 KW obesity; viral infection; bacterial infection; fungal infection;
 KW helminthic infection; protozoal infection; anorexia; cancer;
 KW cardiovascular disease; hypertension; atherosclerosis;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW epilepsy; immune disorder; osteoarthritis; haematopoietic disorder;
 KW inflammatory skin disorder; asthma; dyslipidemia; human; gene; ds.

XX OS Homo sapiens.

XX PN WO2003060149-A2.

XX PD 24-JUL-2003.

XX PF 06-JAN-2003; 2003WO-US000252.

XX PR 04-JAN-2002; 2002US-0345222P.

XX PR 14-JAN-2002; 2002US-0348693P.

XX PR 16-JAN-2002; 2002US-0349182P.

XX PR 17-JAN-2002; 2002US-0349733P.

XX PR 18-JAN-2002; 2002US-0350263P.

XX PR 24-JAN-2002; 2002US-0351977P.

XX PR 28-MAY-2002; 2002US-0383758P.

XX PR 05-JUN-2002; 2002US-0385969P.

XX PR 11-JUN-2002; 2002US-0387834P.

XX PR 17-JUL-2002; 2002US-0396407P.

XX PR 30-SEP-2002; 2002US-0415115P.

XX PR 03-JAN-2003; 2003US-00336603.

XX PA (CURA-) CURAGEN CORP.

XX PI Grosse KM, Alsbrook JP, Anderson DW, Burgess CE, Edinger SR;

XX PI Ellerman K, Furtak X, Gangalli EA, Gerlach VL, Gilbert JA;

XX PI Gunther E, Gorman L, Guo X, Ji W, Li L, Miller CE, Padigar M;

XX PI Patturajan M, Rastelli L, MacDougall JR, Mishra VS, Smithson G;

XX PI Spytek KA, Stone DJ, Shenoy SG, Taupier RJ, Vernet CAM, Zhong M;

XX PI Malyankar UM, Millet I, Kekuda R;

XX

DR WPI; 2003-587288/55.

DR P-PSDB; ADD49065.

XX

PT New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
 PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
 PT asthma, or infections.

XX

PS Claim 20; Page 144; 311pp; English.

XX

CC The present invention relates to novel NOV proteins and their coding
 CC sequences (ADD49028-ADD49131). The proteins and coding sequences are
 CC useful in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease, preferably a NOV-associated disorder
 CC such as metabolic disorders, diabetes, obesity, infectious diseases
 CC (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer,
 CC cardiovascular diseases (hypertension, atherosclerosis),
 CC neurodegenerative disorders (Alzheimer's disease, Parkinson's disease,
 CC epilepsy, immune disorders (osteoarthritis), hematopoietic disorders,
 CC inflammatory skin disorders, asthma and various dyslipidemias. The coding
 CC sequences and proteins may also be used as targets for the identification
 CC of small molecules that modulate or inhibit e.g. neurogenesis, cell
 CC differentiation, cell proliferation, haematopoiesis, wound healing and
 CC angiogenesis, in gene therapy, in generation of antibodies that bind
 CC immunospecifically to NOV substances for use in therapeutic or diagnostic
 CC methods.

XX

SQ Sequence 1611 BP; 448 A; 403 C; 434 G; 326 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 9; Length 1611;

Best Local Similarity 94.1%; Pred. No. 1.7e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCGCGCGCGCGGG 18

Db 116 GCGCGCGCGCGCGGG 132

RESULT 12

ADA69886/c

ID ADA69886 standard; DNA; 2196 BP.

XX AC ADA69886;

XX DT 20-NOV-2003 (first entry)

XX DE Rice gene, SEQ ID 3209.

XX KW Plant; bacterial infection; fungal infection; viral infection; rice;
 KW gene; ds.

XX

OS Oryza sativa.

XX

PN WO2003000898-A1.

XX

PD 03-JAN-2003.

XX

PF 22-JUN-2001; 2001WO-IB001105.

XX

PR 22-JUN-2001; 2001WO-IB001105.

XX

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX

PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX

DR WPI; 2003-175290/17.

XX

PT Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.

XX PS Claim 6; SEQ ID NO 3209; 899pp; English.

CC The present invention relates to a method (M1) for identifying genes

CC involved in plant resistance or response to pathogenic infection. M1

CC comprises identifying a gene whose expression is significantly altered in

CC the incompatible interaction of plant gene expression relative to

CC expression of the gene in an uninfected plant, in a mutant plant that

CC does not express a gene associated with response to pathogenic infection,

CC or in a corresponding incompatible or compatible interaction. (M1) is

CC useful for conferring resistance to resistance or tolerance to a plant to

CC bacterial, fungal or viral infection. The present sequence was used to

CC illustrate the invention.

XX SQ Sequence 2196 BP; 481 A; 542 C; 607 G; 563 T; 0 U; 3 Other;

Query Match 85.6%; Score 15.4; DB 7; Length 2196;

Best Local Similarity 94.1%; Pred. No. 1.6e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGCGGGCGCAGGGGG 18

Db 356 GCGCGGGCGCAGGGGG 340

RESULT 13

ADD29815

ID ADD29815 standard; mRNA; 2448 BP.

XX AC ADD29815;

XX 15-JAN-2004 (first entry)

XX Human tumour suppressor mRNA SEQ ID NO:311.

XX SS; human; tumour suppressor; cancer; cancer; cytostatic; gene therapy.

XX Homo sapiens.

XX WO2003058201-A2.

XX 17-JUL-2003.

XX 31-DEC-2002; 2002WO-US041825.

XX 31-DEC-2001; 2001US-0345317P.

XX (QUAR-) QUARK BIOTECH INC.

XX (CLEV-) CLEVELAND CLINIC FOUND.

XX Feinstein E, Gudkov AV;

XX WPI; 2003-598393/56.

XX Diagnosing cancer comprises determining the polypeptide or polynucleotide

XX levels e.g., hepatic lipase, in a sample from a subject, where a higher

XX level compared to that in a subject free of cancer is indicative of

XX cancer.

XX Disclosure; SEQ ID NO 311; 272pp; English.

XX The invention relates to a novel method for diagnosing a cancer in a

XX subject. The method comprises determining, in a sample from the subject,

XX the level of at least one polypeptide, where a higher level of the

XX polypeptide compared to the level of the polypeptide in a subject free of

XX cancer is indicative of cancer. The polypeptide is selected from any of

XX the polypeptides encoded by the polynucleotides listed in the

XX specification and polypeptides which are at least 70% homologous to the

XX polypeptides. The method of the invention has cytostatic activity, and

XX may have a use in gene therapy. The method is useful in identifying

XX markers specific for one or several types of cancer, depending on the

XX tissue origin, which may be used in numerous diagnostic and prognostic

XX applications as well as cancer type-specific targets for therapeutic

CC intervention. The compounds that modulate the activity of a tumour

CC suppressor gene are useful in the treatment of cancer or as anti-cancer

CC drugs. The present sequence represents a polynucleotide of the invention.

XX SQ Sequence 2448 BP; 573 A; 728 C; 609 G; 522 T; 0 U; 16 Other;

Query Match 85.6%; Score 15.4; DB 9; Length 2448;

Best Local Similarity 94.1%; Pred. No. 1.6e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGCGGGCGCAGGGGG 18

Db 490 GCGCGGGCGCAGGGGG 506

RESULT 14

AAA79707/c

ID AAA79707 standard; cDNA; 2478 BP.

XX AC AAA79707;

XX 27-NOV-2000 (first entry)

XX Eucalyptus grandis cell signalling involved polynucleotide SEQ ID NO:859.

XX Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification;

XX plant cell signalling; modulation; transgenic plant; pathogen; growth;

XX environmental change; development; cell proliferation; differentiation;

XX elongation; survival; disease resistance; nutrient metabolism; ss.

XX Eucalyptus grandis.

XX WO2000042171-A1.

XX 20-JUL-2000.

XX 11-JAN-2000; 2000WO-US000724.

XX 12-JAN-1999; 90US-00228985.

XX 01-NOV-1999; 99US-0162868P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Strabala TJ, Nieuwenhuizen NJ;

XX WPI; 2000-476052/41.

XX Isolated polynucleotide encoding a polypeptide involved in cell signaling

XX used for generating transgenic plants with modified responses to external

XX signals.

XX Claim 1; Page 415-416; 527pp; English.

XX AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide

XX and protein sequences isolated from eucalyptus (Eucalyptus grandis) or

XX pine (Pinus radiata also known as Monterey pine). The protein sequences

XX are involved in cell signalling. The polynucleotide and protein sequences

XX can be used to modify the response of plant cells to external signals

XX e.g. environmental changes or pathogens during the growth and development

XX of a plant. They can be used to modify cell proliferation,

XX differentiation, elongation and survival, resistance to disease and

XX nutrient metabolism. Examples of modifications which can be produced are

XX altered fruit ripening and senescence of leaves and flowers e.g. to delay

XX senescence and prolong the life of cut flowers or enhance senescence of

XX reproductive organs to engineer sterile plants. Other modifications can

XX be used to delay senescence in selected cell types or organs providing

XX fruit and vegetables which have a longer shelf life between harvest and

XX consumption, or to decrease branching frequency in forest tree species

XX giving long stretches of valuable knot-free clear wood which can be used

XX in solid timber furniture and veneers

XX Sequence 2478 BP; 518 A; 756 C; 671 G; 533 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 3; Length 2478;
 Best Local Similarity 94.1%; Pred. No. 1.6e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGCCGCGCAGGGGG 18
 Db 243 GCGCCGCGCAGGGGG 227

Search completed: July 2, 2004, 08:31:38
 Job time : 137.89 secs

RESULT 15
 ADD15216
 ID ADD15216 standard; DNA; 2559 BP.
 XX AC
 AC ADD15216;
 XX AC
 XX AC
 DT 15-JAN-2004 (first entry)
 XX XX
 DE Human serotonin 5-HT2 receptor DNA.
 XX human; ds; mental disorder; differential gene expression; psychosis;
 KW schizophrenia; mood disorder; bipolar; major depression; neuroleptic;
 KW antidepressant; gene therapy.
 XX XX
 OS Homo sapiens.
 XX XX
 FN WC2003039490-A2.
 XX XX
 PD 15-MAY-2003.
 XX XX
 XX 12-NOV-2002; 2002WO-US036683.
 XX XX
 PR 09-NOV-2001; 2001US-0339252P.
 XX XX
 XX (UYTE-) UNIV OFFICE TECHNOLOGY LICENSING STANFORD.
 XX XX
 XX Akil H, Bunney WE, Burke S, Choudary PV, Cox DR, Evans S;
 PI Jones EG, Li J, Lopez JF, Myers RM, Thompson R, Vawter MP;
 PI Watson SJ;
 XX WPI; 2003-441464/41.
 DR XX
 XX XX
 PT Determining a predisposition to mental disorders utilizing differential
 PT gene expression, useful for diagnosing, and/or treating mood disorders or
 PT psychosis, including bipolar and major depression disorders and
 PT schizophrenia.
 XX XX
 PS Example 3; SEQ ID NO 24; 85pp; English.
 XX XX
 CC This invention relates to a novel method for determining a predisposition
 CC to mental disorders by utilising differential gene expression.
 CC Specifically, it refers to the differential gene expression of brain
 CC region specific nucleic acids that can be used to determine a prevalence
 CC of mental disorders with a gender bias. Accordingly, it comprises
 CC contacting a patients biological sample with a reagent (e.g. antibody)
 CC that selectively associates with a polynucleotide given in the
 CC specification, and detecting the level of reagent that associates to
 CC determine whether the subject has, or is predisposed for, a mental
 CC disorder. As such, the present invention describes a method and
 CC compositions that are useful for diagnosing, and/ or treating mental
 CC disorders, such as psychosis e.g. schizophrenia or a mood disorder
 CC including bipolar and major depression disorders. These compositions have
 CC neuroleptic and antidepressant activities and can be used to treat the
 CC aforementioned conditions via gene therapy routes. This polynucleotide
 CC sequence is a brain specific gene (with gender bias) that is
 CC differentially expressed in individuals predisposed to a mental disorder,
 CC used in an exemplification of the invention.
 XX XX
 SQ Sequence 2559 BP; 579 A; 787 C; 627 G; 566 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 9; Length 2559;
 Best Local Similarity 94.1%; Pred. No. 1.6e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

www-bio.1lnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40ml3 fwd. RT from Amersham
High quality sequence stop: 1.

FEATURES

source

1. 320
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1218808"
/sex="male"
/tissue type="normal prostate"
/lab_host="DH103"
/clone_lib="NCI_CGAP_Pr22"

/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 94.4%; Score 17; DB 9; Length 320;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGCCGATCGAGGGGG 18

Db 68 GCGCCGATCGAGGGGG 52

RESULT 2

BH797911

LOCUS

DEFINITION BH797911 565 bp DNA linear GSS 25-APR-2002
1008096D04.x1 1008 - RescueMu Grid I Zea mays Genomic, Genomic survey sequence.

ACCESSION

VERSION

BH797911.1

GI:20307382

KEYWORDS

GSS.

SOURCE

ORGANISM

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 565)

Walbot,V.

Maize genomic sequences found using engineered RescueMu transposon

Contact: Walbot V

Unpublished (2001)

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site so sequence was trimmed. Post-ligation

sequence submitted separately.

Plate: 1008096 row: 26

Class: transposon-tagged.

Location/Qualifiers

1. 565

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/Al88/B73"

/db_xref="taxon:4577"

/tissue type="leaf"

/dev stage="adult"

/lab_host="DH103"

/clone_lib="1008 - RescueMu Grid I"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site www.zmndb.iastate.edu and follow the links for 'RescueMu'. Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 94.4%; Score 17; DB 28; Length 565;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCCCGATCGAGGGGG 17

Db 521 TCGCCCGATCGAGGGGG 537

RESULT 3

CG254815/c

LOCUS

DEFINITION

CG254815

ACCESSION

VERSION

CG254815.1

KEYWORDS

GSS.

SOURCE

ORGANISM

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 870)

Whitelaw,C.A.; Quackenbush,J.; Van Aken,S.; Uterback,T.; Resnick,A.; Fraser,C.M.; Budiman,M.A.; Bedell,J.A.; Rohlfing,T.; Citek,R.W.; Nunberg,A.; Robbins,D. and Lakey,N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: CG1DX07TV

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1. 870

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone="ZMMB040A14"

/clone_lib="ZM_0.7-1.5_KB"

/note="Vector: pBCKS-; Site 1: HincII; 0.7-1.5 kb

methylation filtered genomic DNA library"

ORIGIN

Query Match 94.4%; Score 17; DB 29; Length 870;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCCCGATCGAGGGGG 17

Db 420 TCGCCCGATCGAGGGGG 404

RESULT 4

CG238619/c

LOCUS	CG238619	877 bp	DNA	linear	GSS 22-AUG-2000							
DEFINITION	CG1AQ39TH ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0719G05, genomic survey sequence.											
ACCESSION	CG238619											
VERSION	CG238619.1	GI:34138505										
KEYWORDS	Zea mays											
ORGANISM	Zea mays											
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.											
AUTHORS	1 (bases 1 to 877) Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.											
TITLE	Consortium for Maize Genomics											
JOURNAL	Unpublished (2002)											
COMMENT	Other GSs: OGI:Q39TV Contact: Cathy Whitelaw											
FEATURES	TIGR 7912 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org Seq Primer: TR Class: sheared ends.											
source	Location/Qualifiers 1..877 /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" /db_xref="taxon:4577" /clone="ZMMBMA0719G05" /clone_lib="ZM 0.7 1.5 KB" /note="vector_pacSk; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"											
ORIGIN	Query Match Best Local Similarity 94.4%; Score 17; DB 29; Length 877; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
Qy	1 TGCGCCGATGCAGGGG 17 											
Db	246 TGCGCCGATGCAGGGG 230 											
RESULT 5												
LOCUS	CG662082	907 bp	DNA	linear	GSS 19-JUN-2003							
DEFINITION	OGBVN58TH ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0496J20, genomic survey sequence.											
ACCESSION	CG662082											
VERSION	CG662082.1	GI:32065965										
KEYWORDS	Zea mays											
SOURCE	Zea mays											
ORGANISM	Zea mays											
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.											
AUTHORS	1 (bases 1 to 907) Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.											
TITLE	Consortium for Maize Genomics											
JOURNAL	Unpublished (2002)											
COMMENT	Other GSs: OGBVN58TV Contact: Cathy Whitelaw											
	TIGR 7912 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org											

```

CC662091
LOCUS       CC662091       964 bp      DNA      linear      GSS 19-JUN-2003
DEFINITION  OGVEN58TV ZM 0.7 1.5 KB Zea mays genomic clone ZM58Ma0496J20,
genomic survey sequence.
ACCESSION   CC662091
VERSION     CC662091.1  GI:32065976
KEYWORDS    GSS.
SOURCE      Zea mays
            Zea mays
ORGANISM    Zea mays
REFERENCE   1  (bases 1 to 964)
AUTHORS     Whiteclaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
            Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
            Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
            Consortium for Maize Genomics
            Unpublished (2002)
            Other GSSs: OGVEN58TH
            Contact: Cathy Whitelaw
TIGR        9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: sheared ends.
FEATURES             Location/Qualifiers
     source           1..964
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZM58Ma0496J20"
                     /clone_lib="ZM 0.7 1.5 KB"
                     /note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
                     methylation filtered genomic DNA library"
ORIGIN
Query Match      94.4%; Score 17; DB 29; Length 964;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCCGCGATGCAGGGGG 17
|||||
Db 733 TCGCCGCGATGCAGGGGG 749

RESULT 8
CC615817
LOCUS       CC615817       972 bp      DNA      linear      GSS 18-JUN-2003
DEFINITION  OGLAP15TV ZM 0.7 1.5 KB Zea mays genomic clone ZM58Ma0310D06,
genomic survey sequence.
ACCESSION   CC615817
VERSION     CC615817.1  GI:31977238
KEYWORDS    GSS.
SOURCE      Zea mays
            Zea mays
ORGANISM    Zea mays
REFERENCE   1  (bases 1 to 972)
AUTHORS     Whiteclaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
            Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
            Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
            Consortium for Maize Genomics
            Unpublished (2002)
            Other GSSs: OGLAP15TH
            Contact: Cathy Whitelaw
TIGR        9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208

```

```

Email: whitelaw@tigr.org
Seq primer: TP
Class: sheared ends.
FEATURES             Location/Qualifiers
     source           1..972
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZM58Ma0310D06"
                     /clone_lib="ZM 0.7 1.5 KB"
                     /note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
                     methylation filtered genomic DNA library"
ORIGIN
Query Match      94.4%; Score 17; DB 29; Length 972;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCCGCGATGCAGGGGG 17
|||||
Db 401 TCGCCGCGATGCAGGGGG 417

RESULT 9
BQ307583
LOCUS       BQ307583       520 bp      mRNA      linear      EST 16-MAY-2002
DEFINITION  MR0-BT4507-220601-201-h03 BT4507 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BQ307583
VERSION     BQ307583.1  GI:20844024
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (Bases 1 to 520)
REFERENCE   1  (Bases 1 to 520)
AUTHORS     Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
            Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
            Goldman, G.H., deAlmeida, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
            Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
            O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
            Simpson, A.J.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
            20202663
            PUBMED
            10737800
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0at2=MR0-BT4507-
            220601-201-h03at3=2001-06-22at4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 124.
            Location/Qualifiers
            1..520
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /dev_stage="Adult"
            /clone_lib="BT4507"
            /note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:
            SmaI; A mini-library was made by cloning products derived
            from ORESTES PCR (U.S. Letters Patent application No.
            196,716 - Ludwig Institute for Cancer Research) profiles
            into the pUC 18 vector. Reverse transcription of tissue

```


mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 91.1%; Score 16.4; DB 13; Length 520;
Best Local Similarity 94.4%; Pred. No. 9.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCCCGATCGAGGGGG 18
|||||
Db 383 TCGCCCGCTCGAGGGGG 400

RESULT 10

CD507147 1208 bp mRNA linear EST 12-JUN-2003
CDAB3-C07-yld-s SHGC-CDA Gasterosteus aculeatus cDNA clone
CDAB3-C07 3', mRNA sequence.

ACCESSION

CD507147 GI:31437716

KEYWORDS

Gasterosteus aculeatus (three spined stickleback)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.

REFERENCE

1 (bases 1 to 1208)
Kingsley, D.M., Feichel, C., Balabandara, S., Grimwood, J., Dickson, M.,
Schmutz, J. and Myers, R.M.

TITLE

Expressed sequence tags from *Gasterosteus aculeatus*

JOURNAL

Unpublished (2003)

COMMENT

HHMI and Department of Developmental Biology
Stanford University School of Medicine
Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA
Tel: 650 725 5954
Fax: 650 725 7739
Email: kingsley@cngm.stanford.edu

FEATURES

source

1..1208
/organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/strain="Salinas river, CA"
/db_xref="taxon:69293"
/clone="CDA83-C07"
/sex="mixed male and female"
/tissue_type="heads and internal organs combined"
/dev_stage="adult"
/clone_lib="SHGC-CDA"
/notes="Vector: lambda ZAP Express/pBK-CMV; Site 1: EcoRI
(5' adaptor); Site 2: XhoI (3' linker primer). The mixed
organ cDNA library was generated using the ZAP-cDNA method
by Stratagene. First strand cDNA synthesis was primed with
a 50 bp linker primer containing an oligo dT sequence
preceded by a synthetic XhoI site. 5 prime adaptors were
used containing an EcoRI cohesive end. The finished cDNAs
were inserted in to the ZAP express vector
unidirectionally in the sense orientation with respect to
the lacZ promoter of pBK-CMV. An amplified library was
prepared from approximately 3 million primary clones in
the lambda ZAP Express vector. In vivo excision was then
used to generate individual pBK-CMV phagemid clones for
EST sequencing."

ORIGIN

Query Match 91.1%; Score 16.4; DB 14; Length 1208;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCCCGATCGAGGGGG 18
|||||
Db 336 TCGCCCGATCGAGGGGG 353

RESULT 11

LOCUS

CD255841/C

DEFINITION

IMAGE:6954538 5', mRNA sequence.

ACCESSION

CD255841

VERSION

CD255841.1

KEYWORDS

EST.

SOURCE

Xenopus laevis (African clawed frog)

ORGANISM

Xenopus laevis

REFERENCE

1 (bases 1 to 1241)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov

Tissue Procurement:

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM14578 Row: j Column: 09

High quality sequence start: 94

High quality sequence stop: 384.

FEATURES

source

1..1241
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6954538"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD XGC Brnl"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."

ORIGIN

Query Match 91.1%; Score 16.4; DB 14; Length 1241;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1 TCGCCCGATCGAGGGGG 18

Db

855 TCGCCCGATCGAGGGGG 838

RESULT 12

LOCUS

CK245128

DEFINITION

EST728765 potato callus cDNA library, normalized and full-length

Solanum tuberosum cDNA clone POCAB91 3' end, mRNA sequence.

ACCESSION

CK245128

VERSION

CK245128.1

KEYWORDS

EST.

SOURCE

Solanum tuberosum (potato)

ORGANISM

Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CD255841 1241 bp mRNA linear EST 22-MAY-2003
AGENCOURT 14156934 NICHD_XGC_Brnl Xenopus laevis cDNA clone
IMAGE:6954538 5', mRNA sequence.

CD255841

CD255841.1 GI:31016307

EST.

Xenopus laevis (African clawed frog)

Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

Xenopodinae; Xenopus.

1 (bases 1 to 1241)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabs-r@mail.nih.gov

Tissue Procurement:

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM14578 Row: j Column: 09

High quality sequence start: 94

High quality sequence stop: 384.

FEATURES

Location/Qualifiers

1..1241
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6954538"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD XGC Brnl"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."

Query Match 91.1%; Score 16.4; DB 14; Length 1241;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1 TCGCCCGATCGAGGGGG 18

Db

855 TCGCCCGATCGAGGGGG 838

RESULT 12

LOCUS

CK245128

DEFINITION

EST728765 potato callus cDNA library, normalized and full-length

Solanum tuberosum cDNA clone POCAB91 3' end, mRNA sequence.

ACCESSION

CK245128

VERSION

CK245128.1

KEYWORDS

EST.

SOURCE

Solanum tuberosum (potato)

ORGANISM

Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.
 1 (bases 1 to 322)
REFERENCE
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
TITLE Generation of ESTs from potato callus tissue
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST728763 EST728764
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 Clones can be requested from TIGR via potato@tigr.org
 Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
FEATURES
 source
 1..322
 Location/Qualifiers
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="POCA991"
 /tissue_type="callus"
 /lab_host="DH10B-Tona"
 /clone_lib="potato callus cDNA library, normalized and full-length"
 /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."
ORIGIN
 Query Match 88.9%; Score 16; DB 14; Length 322;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 CGCCGATCGAGGGGG 18
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 DB 228 CGCCGATCGAGGGGG 243
 |||||
RESULT 13
LOCUS BF140016/c
DEFINITION 601791154F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4021788 5', mRNA sequence.
ACCESSION BF140016
VERSION BF140016.1 GI:110979056
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 595)
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLN5277 row: 1 column: 13
 High quality sequence stop: 584.
 Location/Qualifiers
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 /mol_type="mRNA"
 /strain="Czech II"
 /db_xref="taxon:10090"
 /clone="IMAGE:4021788"
 /tissue_type="tumor, metastatic to mammary"

/lab_host="DH10B"
 /clone_lib="NCI_CGAP_Lu30"
 /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies.
 Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 88.9%; Score 16; DB 10; Length 595;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGCGGATCGAGGGGG 17

DB 391 CGCGGATCGAGGGGG 376

RESULT 14**LOCUS** BS522625/c**DEFINITION** BS522625 RIKEN full-length enriched, 15 days embryo head Mus musculus cDNA clone D93008K19 3', mRNA sequence.**ACCESSION** BS522625**VERSION** BS522625.2 GI:16443700**KEYWORDS** EST.**SOURCE** Mus musculus (house mouse)**ORGANISM** Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 691)

REFERENCE**AUTHORS** Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shirahashi, F., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, T., Tanaka, Y., Tanaka, T., Toyota, T., Muramatsu, M., and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished (2001)

TITLE On Jul 28, 2000 this sequence version replaced gi:9574083.**JOURNAL** Contact: Yoshihide Hayashizaki**COMMENT** Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@sc.riken.go.jp,

URL: <http://genome.gsc.riken.go.jp/>

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matakichi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunara, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

```

FEATURES
source
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="D930008K19"
/sex="mixed"
/tissue_type="head"
/dev_stage="15 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 15 days embryo
head"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTCTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by the
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGAGAGATTCGAGTATTAATAATTAATCCCCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
gt10"

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ORIGIN
      38.9%; Score 16; DB 10; Length 691;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCCCGCATGCAGGG 16
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Db 161 TGCCCGCATGCAGGG 146

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RESULT 15
CNS040FA
LOCUS 1063 bp DNA linear GSS 01-SEP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 072G316 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION AL268831
VERSION AL268831.1 GI:7990695
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodontinae; Tetraodon.

REFERENCE	1	Tetracodonidae, Tetracodontinae, Tetracodon.
AUTHORS		Roest Croliius, H., Jallou, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Pizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
TITLE		Estimate of human gene number provided by genome-wide analysis using Tetracodon nigroviridis DNA sequence
JOURNAL		Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE		20296633
PUBMED		10835645
REFERENCE	2	
AUTHORS		Roest Croliius, H., Jallou, O., Dasilva, C., Ozouf-Costaz, C., Pizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,

TITLE	Saurin, W., Bernot, A. and Weissenbach, J.
JOURNAL	Characterization and repeat analysis of the compact genome of the
MEDLINE	freshwater pufferfish Tetraodon nigroviridis
PubMed	Genome Res. 10 (7), 939-949 (2000)
REFERENCE	20359837
	10899143
	3 (bases 1 to 1063)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
	- Web : www.genoscope.cns.fr)
COMMENT	This sequence is a single read and was generated as part of a large
	scale clone-end sequencing project of the Tetraodon nigroviridis
	genome. For more information, please take a look at
	http://www.genoscope.cns.fr/Tetraodon .

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FEATURES
  source
    Location/Qualifiers
      generation
        http://...
      i
        .1063
      organism
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      mol_type
        "genomic DNA"
      db_xref
        "taxon:99883"
      clone
        "072G16"
      clone_lib
        "G"
      notes
        "Genoscope sequence ID : COBG072BD08SP1-end :
        pnc-ori"

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ORIGIN
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      Best Local Similarity 83.3%;   Pred. NO. 2.2e+04;
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Qy  1  TGCGCGCATGCAGGGGGG 18
      |||||
Db  101 TGCGCGCATKCTGGGGGG 118

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Search completed: July 2, 2004, 13:33:08
Job time : 1351.14 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:09:30 ; Search time 28.2073 Seconds
(without alignments)
354.132 Million cell updates/sec

Title: US-10-068-160-17
Perfect score: 18
Sequence: 1 tgcgcggcgagggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCOTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	88.9	963	4	US-09-252-991A-7939
2	16	88.9	1050	4	US-09-252-991A-7799
3	14.8	82.2	246	4	US-09-382-552-59
4	14.8	82.2	426	4	US-09-252-991A-3760
5	14.8	82.2	774	4	US-09-489-039A-1478
C 6	14.8	82.2	885	4	US-09-252-991A-16564
C 7	14.8	82.2	1110	4	US-09-489-039A-6658
C 8	14.8	82.2	1169	4	US-09-620-312D-951
C 9	14.8	82.2	1230	4	US-09-489-039A-6246
C 10	14.8	82.2	1251	4	US-09-252-991A-16454
C 11	14.8	82.2	1256	3	US-09-318-448-42
C 12	14.8	82.2	1289	4	US-09-252-991A-16036
C 13	14.8	82.2	1273	3	US-09-318-448-45
C 14	14.8	82.2	1275	3	US-09-318-448-41
C 15	14.8	82.2	1473	4	US-09-252-991A-13784
C 16	14.8	82.2	1500	4	US-09-252-991A-13688
C 17	14.8	82.2	1749	4	US-09-516-914-22
C 18	14.8	82.2	1908	3	US-09-318-448-36
C 19	14.8	82.2	1933	4	US-09-252-991A-3804
C 20	14.8	82.2	2289	4	US-09-489-039A-2837
C 21	14.8	82.2	2355	4	US-09-252-991A-3845
C 22	14.8	82.2	2451	4	US-09-489-039A-3349
C 23	14.8	82.2	2523	4	US-09-489-039A-3473
C 24	14.8	82.2	3359	4	US-09-023-655-1229
C 25	14.8	82.2	4157	4	US-09-252-991A-3666
C 26	14.8	82.2	5771	4	US-09-833-381-307
C 27	14.8	82.2	5915	4	US-09-382-552-3

28	14.8	82.2	6240	4	US-09-382-552-117	Sequence 117, Appl
29	14.8	82.2	6909	4	US-09-382-552-21	Sequence 21, Appl
30	14.8	82.2	6910	4	US-09-382-552-15	Sequence 15, Appl
31	14.8	82.2	6911	4	US-09-382-552-1	Sequence 1, Appl
32	14.8	82.2	6911	4	US-09-382-552-14	Sequence 14, Appl
33	14.8	82.2	6911	4	US-09-382-552-16	Sequence 16, Appl
34	14.8	82.2	6911	4	US-09-382-552-17	Sequence 17, Appl
35	14.8	82.2	6911	4	US-09-382-552-18	Sequence 18, Appl
36	14.8	82.2	6911	4	US-09-382-552-19	Sequence 19, Appl
37	14.8	82.2	6911	4	US-09-382-552-20	Sequence 20, Appl
38	14.8	82.2	6912	4	US-09-382-552-13	Sequence 13, Appl
C 39	14.8	82.2	10348	2	US-08-457-273B-41	Sequence 41, Appl
C 40	14.8	82.2	10348	3	US-08-556-419-13	Sequence 13, Appl
C 41	14.8	82.2	10348	3	US-09-041-886-14	Sequence 14, Appl
C 42	14.8	82.2	10366	1	US-08-246-982A-5	Sequence 5, Appl
C 43	14.8	82.2	10366	1	US-08-453-265-5	Sequence 5, Appl
C 44	14.8	82.2	10906	4	US-08-976-259-63	Sequence 63, Appl
C 45	14.8	82.2	14272	4	US-09-516-914-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-09-252-991A-7939
; Sequence 7939, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7939
; LENGTH: 963
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7939

Query Match 88.9%; Score 16; DB 4; Length 963;
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0;
Qy 3 CCGCGCGCGCGCGGGG 18
Db 906 CCGCGCGCGCGCGGGG 921

RESULT 2
US-09-252-991A-7799
; Sequence 7799, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7799
; LENGTH: 1050
; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7799

Query Match 88.9%; Score 14.8; DB 4; Length 1050;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCGCGCGCAGGGGG 18
|||||
DB 1010 CGCGCGCGCAGGGGG 1025

RESULT 3

US-09-382-552-59

; Sequence 59, Application US/09382552

; Patent No. 6673909

; GENERAL INFORMATION:

; APPLICANT: Brown, Jr., Robert H.

; APPLICANT: Liu, Jing

; APPLICANT: Aoki, Masashi

; APPLICANT: Ho, Meng

; APPLICANT: Matsuda-Asada, Chie

; TITLE OF INVENTION: DYSFERLIN, A GENE MUTATED IN DISTAL MYOPATHY AND LIMB

; FILE REFERENCE: 00786/399002

; CURRENT APPLICATION NUMBER: US/09/382,552

; CURRENT FILING DATE: 1999-08-25

; EARLIER APPLICATION NUMBER: US 60/097,927

; NUMBER OF SEQ ID NOS: 233

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 59

; LENGTH: 246

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-382-552-59

Query Match

Best Local Similarity 82.2%; Score 14.8; DB 4; Length 246;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCGCGCGCGCAGGGGG 18
|||||
DB 163 TCGCGCTGGCGCAGGGG 180

RESULT 4

US-09-252-991A-3760

; Sequence 3760, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 3760

; LENGTH: 426

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-3760

Query Match

Best Local Similarity 82.2%; Score 14.8; DB 4; Length 426;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCGCGCGCGCAGGGGG 18

DB 124 TGCGCGCGCGCAGGGGG 141
|||||

RESULT 5

US-09-489-039A-1478

; Sequence 1478, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 1478

; LENGTH: 774

; TYPE: DNA

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-1478

Query Match

Best Local Similarity 82.2%; Score 14.8; DB 4; Length 774;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCGCGCGCGCAGGGGG 18
|||||
DB 570 TCGCGTGGCGCAGGGGG 587

RESULT 6

US-09-252-991A-16564/c

; Sequence 16564, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 16564

; LENGTH: 885

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-16564

Query Match

Best Local Similarity 82.2%; Score 14.8; DB 4; Length 885;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCGCGCGCGCAGGGGG 18
|||||
DB 311 TGCGCGCGCGCAGGGGG 294

RESULT 7

US-09-489-039A-6658/c

; Sequence 6658, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6658
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6658

Query Match 82.2%; Score 14.8; DB 4; Length 1110;
Best Local Similarity 88.9%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGGCGCGCGCAGCGGGG 18
|||||
Db 1031 TGGCGCTGCGCAAGGGG 1014

RESULT 8

US-09-620-312D-951
; Sequence 951, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yuning
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662al Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 951
; LENGTH: 1169
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (258)..(821)
US-09-620-312D-951

Query Match 82.2%; Score 14.8; DB 4; Length 1169;
Best Local Similarity 88.9%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGGCGCGCGCAGCGGGG 18
|||||
Db 124 TGGCGCGCGCGCGGGG 141

RESULT 9

US-09-489-039A-6246/c

; Sequence 6246, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Bregon et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6246
; LENGTH: 1230
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6246

Query Match 82.2%; Score 14.8; DB 4; Length 1230;
Best Local Similarity 88.9%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGGCGCGCGCAGCGGGG 18
|||||
Db 62 TGGCGCGCGCAGCGGGG 45

RESULT 10

US-09-252-991A-16454/c
; Sequence 16454, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16454
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16454

Query Match 82.2%; Score 14.8; DB 4; Length 1251;
Best Local Similarity 88.9%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGGCGCGCGCAGCGGGG 18
|||||
Db 693 TGGCGCGCGCATGGGCG 676

RESULT 11

US-09-318-448-42
; Sequence 42, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Stenroos, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
; FILE REFERENCE: 601-1-057
; CURRENT APPLICATION NUMBER: US/09/318,448
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 42

Search completed: July 2, 2004, 13:37:41
Job time : 29.2073 secs

Sequence 5, Application US/10666022
Publication No. US20040105872A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the
APPLICANT: Secretary of the Department of Health and Human Services
APPLICANT: Kinnman, Dennis W.
APPLICANT: Vertheim, Daniela
TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
SUBJECTS WITH IMMUNOSTIMULATORY CPG
FILE REFERENCE: 4239-66899
CURRENT APPLICATION NUMBER: US/10/666,022
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,944
PRIOR FILING DATE: 2002-09-18
NUMBER OF SEQ ID NOS: 181
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic
FEATURE:
NAME/KEY: misc feature
LOCATION: {1}..(20)
OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-5

Query Match 100.0%; Score 18; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCGCGCGCGCAGGGGG 18
|||||
Db 3 TCGCGCGCGCGCAGGGGG 20

RESULT 3
US-10-437-963-58926/c
Sequence 58926, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 58926
LENGTH: 687
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_60597C.1
US-10-437-963-58926

Query Match 91.1%; Score 16.4; DB 17; Length 687;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCGCGCGCGCAGGGGG 18
|||||
Db 204 TCGCGCGCGCGCAGGGG 187

RESULT 4
US-10-437-963-55777/c
Sequence 55777, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 55777
LENGTH: 2052
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_57751C.1
US-10-437-963-55777

Query Match 88.9%; Score 16; DB 17; Length 2052;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGCGCGCGCAGGGGG 17
|||||
Db 272 GCGCGCGCGCAGGGGG 257

RESULT 5
US-10-437-963-3377/c
Sequence 3377, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 3377
LENGTH: 369
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_10359C.1
US-10-437-963-3377

Query Match 85.6%; Score 15.4; DB 17; Length 369;
Best Local Similarity 94.1%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCGCGCGCAGGGGG 18
|||||
Db 280 GCGCGCGCGCAGGGGG 264

RESULT 6


```
RESULT 10
US-10-437-963-22077
; Sequence 22077, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 22077
; LENGTH: 616
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_27287C.1
US-10-437-963-22077

Query Match      85.6%; Score 15.4; DB 17; Length 616;
Best Local Similarity 94.1%; Pred. No. 5.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCGCGCGCAGCGGGG 18
DB 282 GCGCGCGCGCAGCGGG 298

RESULT 11
US-10-198-846-7873/c
; Sequence 7873, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7873
; LENGTH: 664
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 16, 432, 474, 499, 500, 504, 516, 522, 523, 524, 531, 547,
; LOCATION: 548, 556, 568, 569, 578, 593, 594, 597, 612, 614,
; LOCATION: 620, 621, 628, 634, 637
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-7873

Query Match      85.6%; Score 15.4; DB 15; Length 664;
Best Local Similarity 94.1%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCGCGCGCAGCGGGG 18
```

```
DB 295 GCGCGCGCGCATGGGG 279

RESULT 12
US-10-259-165-431/c
; Sequence 431, Application US/10259165
; Publication No. US2003013588A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Rickes, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 431
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-165-431

Query Match      85.6%; Score 15.4; DB 15; Length 681;
Best Local Similarity 94.1%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCGCGCGCAGCGGGG 17
DB 637 TCGCGCGCGCAGCGGGG 621

RESULT 13
US-10-259-165-99/c
; Sequence 99, Application US/10259165
; Publication No. US2003013588A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Rickes, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
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; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 99
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-165-99

Query Match      85.6%; Score 15.4; DB 15; Length 684;
Best Local Similarity 94.1%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCCTCGGCGCAGGGG 17
   |||||
Db 637 TGCCTCGGCGCAGGGG 621

RESULT 14
US-10-198-846-11115/C
; Sequence 11115, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11115
; LENGTH: 745
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11115

Query Match      85.6%; Score 15.4; DB 15; Length 745;
Best Local Similarity 94.1%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCCTCGGCGCAGGGG 18
   |||||
Db 297 GCCTCGGCGCAGGGG 281
```

```
RESULT 15
US-10-425-114-2950
; Sequence 2950, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
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```
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2950
; LENGTH: 785
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700237916_FLI
US-10-425-114-2950

Query Match      85.6%; Score 15.4; DB 13; Length 785;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCCTCGGCGCAGGGG 17
   |||||
Db 113 TGCCTCGGCGCAGGGG 129

Search completed: July 2, 2004, 13:58:25
Job time : 138.732 secs
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